

FIGURE 1

CGGACGCGTGGGTGCGAGGCAGGGTACCGAGCATTCACTGCTCGGTAGA
 CCTGGTGCACCACCACCA**TG**TTGGCTGCAAGGCTGGTGTCTCCGGACACTACCTTAGG
 GTTTCCACCCAGCTTCACCAAGGCCTCCCTGTTGAAGAAATTCCATCACGAAGAACATCA
 ATGGCTGTTAACACCTAGCAGGGAAATGCCACCAAAAACAAGAAATTGGGATCCGGCGTGGGA
 GAACTGGCCAAGAACTCAAAGAGGCAGCATGGAACCATCGATGGAAAAAATATTAAAATT
 GATCAGATGGGAAAGATGGTTGTTGCTGGAGGGCTGCTGTTGGCTTGGAGCATTGTGCTA
 CTATGGCTTGGACTGTCTAACGAGATTGGAGCTATTGAAAAGGCTGTAATTGGCCTCAGT
 ATGTCAAGGATAGAATTCCACCTATATGTAAGCAGGGAGTATTGGTTAACAGCT
 TTGTCGCCATAGCAATCAGCAGAACGCCTGTTCTGAACTTCACTGATGAGAGGGCTTTG
 GGTGACAATTGGTGTGACCTTGCAAGCCATGGTGGAGCTGGAATGCTGGTACGATCAATA
 CATATGACCAGAGGCCAGGCCAAAGCATCTGCTGGTTGCTACATTCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGCTCCTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCCTCTCCACTGTTGCCATGTGCGCCCAGTGAAAAGTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCTGGTCTCGTCTTGTGTCCTCATGGGATCTATG
 TTTCTCCACCTACCACCGTGGCTGGTGCCTTACTCAGTGGCAATGTACGGTGGATT
 AGTTCTTCAGCATGTTCTCTGTATGATAACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTTCAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTAATATATTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAA**TG**
AAGTGACTCAGCTCTGGCTCTGCTACATCAAATATCTGTTAATGGGGCAGATATGC
 ATTAAATAGTTGTACAAGCAGCTTCGTTGAAGTTAGAAGATAAGAACATGTCATCATA
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTCTGGAGAATAATGCAGT
 AATCCTCTCCAAATAAGCACACACATTTCATTCTCATGTTGAGTGTGATTAAATGTT
 TTGGTGAATGTGAAAACCTAAAGTTGTCATGAGAATGTAAGTCTTTCTACTTTAAA
 TTTAGTAGGTTCACTGAGTAACCTAAATTAGCAAACCTGTGTTGCATATTGGAGT
 GCAGAATATTGTAATTATGTCATAAGTGAATTGGAGCTTGGTAAAGGGACCAGAGAGAAG
 GAGTCACCTGCAGTCTTGTGTTAAATACTTAGAACTTAGCACTGTGTTATTGATTA
 GTGAGGAGCCAGTAAGAACATCTGGGTATTGGAAACAAGTGGTCATGTTACATTCTT
 GCTGAACCTAACAAAACGTTCATCCTGAAACAGGCACAGGTGATGCATTCTCCTGCTGTTG
 CTTCTCAGTGCTCTTCCAATATAGATGTTGTCATGTTGACTGTACAGAATGTTAAC
 ATACAGAGAACCTTGATGGAATTATATATGTTGTTACTTTGAATGTTACAAAAGGAA
 ATAACCTTAAACTATTCTCAAGAGAAAATTCAAAGCATGAAATATGTTGCTTTCCAG
 AATACAAACAGTATACTCATG

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGGRWFVAGGAAVGLGALCYGLGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWTIGVTFAAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTI^LGGLI^RA^WYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGIVLFSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLS^IYMDTLN^IFMRVATMLATGGNRKK

FIGURE 3

GAAGGCTGCCTCGTGGTCCGAATCGGTGGCGCACGTCCGCCGTCCTCGCCTCTGCAT
 CGCGGCTTCGGCGGCTTCACCTAGACACCTAACAGTCGCGGAGCCGGCGTCGTGAGGG
 GGTGGCACGGGGAGTCGGCGGTCTTGTGCATCTGGCTACCTGTGGTCGAAG**ATG**TGG
 ACATCGGAGACTGGTTAGGAGCATCCGGCGATACGCGCTATTGGTCGCCGCCACCGTC
 GCCGTGCCCTTGGTCGGCAAACCTCGGCCTCATCAGCCGGCTACCTCTCTGGCCCGA
 AGCCTCCTTATCGCTTCAGATTGGAGGCCAATCACTGCCACCTTATTCCCTGTGG
 GTCCAGGAAGTGGATTCTTATTGGTCAATTATATTCTATATCAGTATTCTACGCGA
 CTTGAAACAGGAGCTTGATGGAGGCCAGCAGACTATTATCATGTCCTTTAACCTG
 GATTGATCGTGAATTACTGGCTAGCAATGGATATGCAGTTGCTGATGATTCCCTGATCA
 TGTCAGTACTTTATGTCGGGCCAGCTGAACAGAGACATGATTGTATCATTGGTTGGA
 ACACGATTAAAGGCCGCTATTACCCGGTTATCCTGGGATTAACATATATCGGGAGG
 CTCGGTAATCAATGAGCTATTGAAATCTGGTGGACATCTTATTCTTAATGTTCA
 GATAACCAATGGACTTGGAGGAAGAAAATTCTATACACACTCAGTTTGTACCGCTGG
 CTGCCAGTAGGAGAGGGAGTATCAGGATTGGTGTGCCCTGCTAGCATGAGGCGAGC
 TGCTGATCAGAATGGCGGGAGGCGGGAGACACAACACTGGGCCAGGGCTTCGACTGGAGACC
 AG**TGA**AGGGCGGCCCTGGCAGCGCTCTCAAGCCACATTCTCCAGTGCTGGGTG
 CACTAACAACTGCGTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTA
 AGTACGAGACAAAGTTCTAAATCCGAAGAAAAATAAAGTGTCCACAAGTTCACGAT
 TCTCATTCAGTCCTACTGCTGTGAAGAACAAATACCAACTGTGCAAATTGCAAAACTGAC
 TACATTTTGGTGTCTCTCTCCCCTTCCGCTGAATAATGGGTTTAGCGGGTCT
 AATCTGTCGGCATTGAGCTGGGCTGGGTACACAAACCCCTTCCAAAAGGACCTATCT
 TCTTGACACATGCCCTCTCCCACATTCCCAACCCCCACATTGCAACTAGAAAAGTG
 CCCATAAAATTGCTCTGCCCTGACAGGTTGTTATTGACTTTGCCAAGGCTGGT
 ACAACAAATCATATTACGTTTCCCTTGGTGGCAGAACACTGTTACCAATAGGGGGAG
 AAGACAGCCACGGATGAAGCGTTCTCAGCTTGGATTGCTGACTGACATCCGTTGTT
 AACCGTTGCCACTCTCAGATATTATAAAAAAGTACCAACTGAGTTCATGAGGGCCA
 CAGATTGGTTATTAAATGAGATACGAGGGTTGGTGTGGGTGTTGTTCTGAGCTAAGTGA
 TCAAGACTGTAGGGAGTGCAGCTAACATGGTTAGGTTAAACCATGGGGATGCACCC
 TTTGCGTTTCAATGTACTGCCCTACTGGTTGTAGCTGGAGTAGTTGGGTGCTTGTT
 TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTTGTGAGAGGTCTGGG
 ATTCCCATTCATCTCATTGGATATGTTGTCATGAGTAAAGGAGGAGAGACCCCTCAT
 CGCTATTAAATGTCATTGGCTATCCCCGTTTGGTCAATTAAAGCTAATGTA
 GAGGAAGGCGCAGCTCTCTGCACGTTAGATCATTAAAGCTAATGTAAGCACATCTA
 AGGGAAACATGATTAAAGGTTGAAATGGCTTGAATCATTTGGGTTGAGGGTGTGTA
 TTTTGAGTCATGAATGTACAAGCTGTGAATCAGACAGCTAAACACCCACACCTTT
 TCGTAGGTGGCTTCTCATCAGAGCTGGCTCATACCAAAATAAGTTTGAAGGCCA
 TGGCTTTCACACAGTTATTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT
 ATTGAGTGGCTGTCACACTTGAGGCAACTAAAAGGCTCAACAGTTGATCAGTTCT
 TTCAGGAAACATTGCTTAACAGTATGACTATTCTTCCCCACTCTAACAGTGTGAT
 GTGTGTATCCTAGGAAATGAGAGTTGGCAACACAACCTCTCATTTGAATAGAGTTGTG
 TACTTCTCCATTAAATTATGATAAAATAGGTGGGGAGAGTCTGAACCTTAACCTG
 TGTTTGTGTTCATCTGTCACACTCATGTCAGGGCGTGGAGACTCATTGATGTATA
 CCAATTATGTCACACTCATGTCAGGGCGTGGAGACTCATTGATGTATAAGAATA
 TTTCTGACAGTGAGTGACCCGGAGTCTGTTGACCTCTTACCAAGTCAGCTGCCTG
 CAGTCATTCTTCAAAAGGTTACAAGTATTAGAACCTTCAAGTCAGGGCAAAATGTC
 ATGAAGTTATTCTCTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTGCTGGATT
 ATGTTCTGGAATAATTACAAAAGCTATTGAGTTGACTTGACAAAGGCAAAACA
 TGACAGTGGATTCTCTTACAAATGGAAAAAAATCCTTATTGTATAAAGGACTTCC
 TTTTGAAACTAATCCTTTATTGGTAAAATTGTAAATTAAAGTGCACACTTG

FIGURE 4

MSDIDGWFRSIPAI TRYWFAATVAVPLVGKLG LISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYL FMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWF GTRFKACYLPWVILGFNYIIGGSVINE LIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGCCATAGCGACCATTTGCATTAACGGTTG
 GTAGCTTCTATCCTGGGGCTGAGCGACTGCAGCTCTCCCTACTCCCTCTCGGCT
 CCTTGTGGCCAAAGGCCAACCGGGTCCGGCTCTGGCCTAGGGATCTCCCCGTTGCC
 CCTTGCGGG**ATG**GCTGCGGAAGAAGAAGACGAGGTGGAGTGGTAGTGGAGAGCATCG
 CGGGGTTCCCTGCGAGGCCAGACTGGTCCATCCCCATCTGGACTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTATTGGT
 GCCCTGTGTTCCCTGTTTGATGATGAAGAAGAAAGCAAATTGACCTATAACAGAGATTC
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTCAAGAAGCATGCACTCTCCTCTGCAAAGACCCATACATCACAGGC
 CATTGCAACCTGTGTTGGCAGCAGAAGATTTACTATCTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTGAAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTAACCGATGGCTCTGATGTGGTCAGTGACCTGAAACACGAAGAGATGAAATCCT
 GAGGGAAGTTCTTAGAAATCAAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
 AACAGTTATCAGAGGCTAAACAGAAGAGCCCACAGTCATCCAGTGAAGCTGCAATAATG
 AATAATTCCAAGGGATGGTGAACATTGACACACCACCCCTCAGAAGTTAAATGCATT
 TGCTAATCAGTCAATAGAACCTTGGAAAGAAAAGTGGAAAGGTCTGAAACTCCTCCCTCC
 CACAAAAAGGCCTGAAGATTCCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
 TTATCAGTACTTGGAACAGAACGAACTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGCAGAGAAACTCAAAGAAGAAGTTATTAATAAG**TA**
ATAATTAAGAACAAATTAAACAAATGGAAGTTCAAATTGTCTAAAAATAATTATTAGTC
 CTTACACTG

FIGURE 6

MAAEEEDEVEWVVESIAGFLRGPDWSIPILDFVEQKCEVNCKGGHVITPGSPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAAEDFTIFKAMMVQKNIEMQLQAIRIIQERNGVLPDCLTDGSDVVSDLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEEKQTLLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTGATGATGAAGAAGAAAGCAAATTGACCTATAACAGAGAT
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAACATGAAGATCAATTCAAGAACGATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTGGCAACCTGTGTTGGCAGCAGAAGATTACTATCTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTGAACACGAAGAGATGAAAAT
CCTGAGGGAAAGTTCTTAGAAAATCAAAAGAGGAATATGACCAGGAA

FIGURE 8

GCGTGGTTCTGCAATAGCGGCTAGAGGGAGGGCTTTCCGCCTACACCTACTG
 TAGCTTCTCCACGTATGGACCTAAAGGCTACTGCTGCTACTACGGGGTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGCGTTCTCCACTAGAACGCTTCTGAGGGAGGTAAATTAAAAAC
 AGTGGAA**TG**AAAAAACAGTGCTGTAGTCATCCTGTAATATGCTCCTGTCAACAATGTATAC
 ATTCCCTGCTAGGTGCCATATTCAATTGCTTAAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAACAAGTATGATTCTCCAACACTGTGAATGTGTGCTCAGAACTG
 GTGAAGCTAGTTCTGTGTGCTTGTGTTATAAAGAAAGATCATCAAAGTAG
 AAATTGAAATATGCTCCTGGAAGGAATTCTCTGATTTCATGAAGTGGCCATTCTGCCT
 TTCTTATTCCTGGATAACTTGATTGTCTCTATGCTCTGCTTATCTCAACCAGCCATG
 GCTGTTATCTCTCAAATTAGCATTATAACAAACAGCTCTTCTATTCAAGGATAGTGTGAA
 GAGGCCTCTAAACTGGATCCAGTGGCTCCCTCCTGACTTATTTGTCTATTGTGGCCT
 TGACTGCCGGACTAAAACCTTACAGCACAACTTGGCAGGACGTGGATTTCATCACGATGCC
 TTTTCAGCCCTCCAATTCTGCCTCTTTCAGAAGTGTGAGTGTCCCAGAAAAGACAATTG
 TACAGCAAAGGAATGGACTTTCTGAAAGCTAAATGAAACACACAGCAGAGTTTCAGTC
 ACATCCGTCTGGCATGGCCATGGTCTTATTATAGTCCAGTGTGTTATTCATGGCT
 AATATCTATAATGAAAAGATACTGAAGGGAGGGAACCAGCTACTGAAAGCATCTCATA
 GAACAGCAAACCTTATTCGGCATTCTGTTAATGGGCTGACTCTGGCCTCAGAGGA
 GTAACCGTGTAGATTAAAGAACTGTGGATTTTATGCCACAGTGCTTTAGTGCAG
 CTTATTTGTAACTGCATTCCAGGGCCTTCAGTGGCTTCATTCTGAAGTTCCTGGATAA
 CATGTTCCATGTCTGATGGCCAGGTTACCACTGTCTTACACACAGTGTCTGCTGG
 TCTTGACTTCAGGCCCTCCCTGGAATTCTTCTGGAAGGCCATCAGTCCTCTCTATA
 TTTATTATAATGCCAGCAAGCCTCAAGTCCGGAAATACGACCTAGGAAAGAAAGGATCG
 AGATCTAAGTGGCAATCTTGGAGCGTCCAGTGGGGATGGAGAAGAACTAGAAAGACTA
 CCAAACCCAAGAGTGTGAGTCAGATGAAGATACTTC**TAA**CTGGTACCCACATAGTTGCA
 GCTCTCTGAACCTTATTCACATTTCAGTGTGTTAATATTCTTCACTTGATA
 AACCAGAAATGTTCTAAACCTAAATTCTGATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTAGAGTACCCAAAGGCTAACGAAATTCTAAAGAAACTGATA
 CAGAGGTAACAATGAAGAATTCTAGTACTGATAAACTCAGAAAGTTATGTGAGATTAT
 TTTCTTGGCCTCAAGCTCCAAAAACTTGTAATAATCATGTTAGCTATAGCTTGTATAT
 ACACATAGAGATCAATTGCCAATATTCAACATCATGTTAGTCTAGTTACATGCCAAAGT
 CTTCCCTTTAACATTATAAAAGCTAGGTTGTCTTGAATTGAGGCCCTAGAGATAGT
 CATTGCAAGTAAAGAGCAACGGACCTTCTAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTGGGATGATGTAGTCTGCTAAATATTGCTGAAGAAGCAGT
 TTCTCAGACACAAACATCTCAGAATTAAATTGAGAAATTGATGGAAATTGGATTGT
 AATAATCTTGTGTTAAACATTGGTCCCTAGTCACCATAGTTACCACTTGATTTA
 AGTCATTAAACAAGCCACGGTGGGCTTTCTCCTCAGTTGAGGAGAAAATCTGAT
 GTCATTACTCCTGAATTATTACATTGGAGAATAAGAGGGCATTGTTATTAGTTACT
 AATTCAAGCTGTGACTATTGTTATCTTCAAGAGGTGAAATGCTGGCTTCAGAATCATA
 CAGATTGTCAGTGAAGCTGATGCCTAGGAACCTTAAAGGGATCCTTCAAAAGGATCATT
 AGCAACACATGTTGACTTTAACTGATGTATGAATATTAACTCTAAAGATGAAAGACC
 AGTAATATATAAGTCACCTTACAGTGCTACTCACACTAAAGTGCTGGTATTTCATG
 GTATTTGCATGCAGCCAGTTAACCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA
 AAATTAGCAAACAAAAGTGAATTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAACTGGCAGGCCTGTATGTTACAGACTACCATACTGTAATATGAGCTTATGGTGT
 CATTCTCAGAAACTTATACATTCTGCTCTCCTCTCAGTTGATGCAAGATGAATATA
 AGGTAATATACTATTATAATTCAATTGATCCACAATAATGACTGGCAAGAATTG
 GTGGAAATTGTAATTAAAATAATTAAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNCSELVK
LVFCVLVSFCVIKKDHQSRLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAV
IFSNFSIITTALLFRIVLKRRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
SPSNCLLFRSECPRKDNCATAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
YNEKILKEGNQLTESIFIQNQSKLYFFGILFNGLTGLQRSNRDQIKNCGFFYGHSAFSVALI
FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI
YNASKPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGCTTTCCAATCCGGACGTAATCGTGGTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGCTTTGCCTATACTACTGTAGCTTCTCAC
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCCTTCTTCCACTAGAAGCTCTGAGGGAGGTAATTAAAAAACAGTGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATACATTCTGCTAGG
TGCCATATTGCTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGCATTCTGTGTTATAAGAAAGATCATCAAAGTAGAAATTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTCATGAAGTGGTCCATTCCCTGCCTTCTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCCATCTCAACCAGCCATGGCTGTTATCTC
TCAAATTTAGCATTATAAACACAGCTCTTCTATTCAAGGATAGTGTGAAGAGGGGTCTAAA
CTGGATCCAGTGGGCTTCCCTGACTTTATTTGTCTATTGTGGCCTGACTGCCGGGA
CTAAAACCTTA

FIGURE 11

CGGACGCGTGGCGGACGCGTGGCGGACGCGTGGGCCGGCTGGCTAGCGCGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCTGCGGGCAGAGGAGCAT
 CCCGTCTACCAGGTCCAAGCGCGTGGCCCGGGTCATGGCAAAGGAGAAGGCAGCGAG
 AGCGGCTCCGGGGCTGCTACCCACCAGCATCCTCAAAGCACTGAACGCCGGCCA
 GGTGAAGAAAGAACGAAAAAGAAGAACAAACAGTTGTCTGTTGCAACAAGCTTGCTATG
 CACTGGGGAGCCCCCTACAGGTGACGGCTGTGCCCTGGTTCTCCTCAGATCTAC
 CTATTGG**ATGT**GGCTCAGGTGGCCCTTCTGCCTCCATCATCCTGTTGTGGCGAGC
 CTGGGATGCCATCACAGACCCCTGGTGGCCTTGATCAGCAAATCCCCCTGGACCTGCC
 TGGGTCGCCTATGCCCTGGATCATCTTCTCCACGCCCTGGCGTCATTGCCTACTTCCTC
 ATCTGGTCGTGCCGACTTCCCACACGCCAGACCTATTGGTACCTGCTTTCTATTGCCT
 CTTGAAACAATGGTCACGTGTTCCATGTTCCACTCGGCTCTCACCAGTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACGCCCTATGGATGACTGTGAAAGTGTGGCAC
 AGTGCTGGCAGGGCGATCCAGGGACAAATCGTGGCCAAGCAGACACGCCCTGTTCCAGG
 ACTTCAATAGCTCTACAGTAGCTTACAAAGTGCCAACCATACACATGGCACCACTTCACAC
 AGGGAAACGAAAGGCATACCTGCTGGCAGCGGGGTCTTGTATCTATATAATCTG
 TGCTGTCATCCTGATCCTGGCGTGCAGGAGCAGAGAGAACCTATGAAGCCCAGCAGTC
 AGCCAATCGCCTACTTCCGGGCCTACGGCTGGTATGAGCCACGCCATACATCAAACCT
 ATTACTGGCTCCCTTCACCTCCTGGCTTCTGCTGGGAGGAACTTTGTCTTGT
 TTGCACCTACACCTTGGCTTCCGCAATGAATTCCAGAATCTACTCCTGCCATATGCTCT
 CGGCCACTTAACCATTCCATCTGGCAGTGGTCTTGACCCGGTTGGCAAGAACAGACT
 GTATATGTTGGGATCTCATCAGCAGTGCCTTCTCATCTGGTGGCCCTCATGGAGAGTAA
 CCTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTAC
 TACCTGGTCCATGCTGCCATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCATCTTCTTCTATGTCTTCCATCAAGTTGCCTGGAGTGT
 ACTGGGCAATTCTACCTCAGTCTGGACTTGCAGGGTACCAAGACCCGTGGCTGCTCGCAGC
 CGAACGTGTCAAGTTACACTGAACATGCTCGTACCATGGCTCCATAGTTCTCATCCTG
 CTGGCCTGCTGCTCTCAAAATGTACCCATTGATGAGGAGAGGCGGCCAGAATAAGAA
 GCCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTGGCTGTCAGAACAGACTCCACAG
 AGCTGGCTAGCATCCTC**TAG**GGCCGCCACGTTGCCGAAGCCACCATGCAGAACGCCACAG
 AAGGGATCAGGACCTGTCTGCCGGCTTGCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCAGGACACTTGTGCTGCTACTGTGGGCCGGCTGCTCTG
 TGGCCTCTGCCTCCCTGCCTGCCTGTGGGCCAAGGCCCTGGGCTGCCACTGTGAATA
 TGCCAAGGACTGATGGGCCTAGCCGGAACACTAATGTAGAACCTTTTACAGAGCC
 TAATTAAATAACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTGTGAGCTA
 TTAATGTTATTAAATTTCATAAAAGCTGGAAAGC

FIGURE 12

MWLRWALSLPPSSCLWAEPGMPSQTPWWASASANPPGPAWVALCPGSSPRWPSSLPTSSSG
SCPTSHTARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQGQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFC
YTLGFRNEFQNLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGIISSAVPFLILVALMESNL
ITYAVAVAAGISVAAAFLLPWMSMLPDVIDDFHLKQPHFHGTTEPIFFSFYVFFTKFASGVSLG
ISTLSDLFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRQNKAL
QALRDEASSSGCSETDSTELASIL

FIGURE 13

GGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCTTGTCTGTATCTATATAATCTGT
GCTGTCTCATCCTGATCCTGGCGTGCAGGGAGCAGAGAGAACCCATTGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGCCTACGGCTGGTCATGAGCCACGGCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTGGCTTCATGCTGGTGGAGGGAACTTGTCTTGT
TGCACACTACACCTGGGCTTCCGCAATGAATTCCAGAACATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATCTGGCAGTGGTTCTTGACCCGGTTGGCAAGAACAGACAGCTG
TATATGTTGGATCTCATCAGCAGTGCCATTCTCATCTTGGTGGCCCTATGGAGAGAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTCCATCTGAAGCAGCCCCACTCCATG
GAACCGAGCCCCAT

FIGURE 14

GGGGCTTCGGGCCAGCGCCAGCGCTAGTCGGTCTGTAAGGATTACAAAAGGTGCAGGT
ATGAGCAGGTCTGAAGACTAACATTGTGAAGTTGTAACAGAAAACCTGTTAGAA**ATGT**
GGTGGTTTCAGCAAGGCCTCAGTTCTCCTTCAGCCCTGTAATTGGACATCTGCTGCT
TTCATATTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGTTACCTTATAT
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTGGGGCAATGCTAAATATTGCGG
CAGTTTATGCATTGCTACCATTATGTTGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
GAGAACGTTATCATCAAATTAAACAAGGCTGGCCTGTACTTGAATACTGAGTTGTTAGG
ACTTTCTATTGTGGCAAACCTCCAGAAAACAACCCTTTGCTGCACATGTAAGTGGAGCTG
TGCTTACCTTGGTATGGGCTCATTATATATGTTGTTCAGACCATCCTTACCAAATG
CAGCCCCAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGGTTATCTGGTGTGG
AGTAAGTGCACTTAGCATGCTGACTTGCTCATCAGTTGCACAGTGGCAATTGGACTG
ATTAGAACAGAAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
ACTGCAGCAGAATGGTCTATGTCATTTCCTTGGTTTCTGACTTACATTGCTGA
TTTCAGAAAATTCTTACGGGTGGAAGCCAATTACATGGATTAAACCTCTATGACACTG
CACCTGCCCTATTAACAATGAACGAACACGGCTACTTCCAGAGATATT**TGA**TGAAAGGAT
AAAATATTCTGTAATGATTATGATTCTCAGGGATTGGGAAAGGTTCACAGAAAGTGTGCTTA
TTCTCTCTGAAATTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
ATCAGGAAACATGAAAGAAGCCATTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA
TTAAAAACACCTATGCCTATACTTTTATCTCAGAAAATAAGTCAAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFIRLLLVIWCGVSALSMTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYIRDQKISLRVEANLHGLTLYD
TAPCPINNERTRLLSRDI

FIGURE 16

CGGACGCTTGGCNGGCCAGCGGCAGCGTAGTCGGTCTGGAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGCTTTCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAAATTCTCTGGTTGTTGAAGCAGT
TACCAAGAACATCTCAACCCTTCCCACAAAGCTAATTGAGTACACGTTCTGTTGAGTACA
CGTTCCCTGTTGATTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTCAGCAAGGCCTCAGTTCCCT
TCAGCCCTTGTAAATTGGACATCTGCTGCTTCATATTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTACCTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCGCGCTGCGTCCCAGGTGCAAGTGAGCTTCGGCTGCCCGCGGG
 CGGGGGTGCAGGCCGAC**ATG**CGCCCGCTTCTCGGCCTCCTCTGGTCTCGCCGGCTGCAC
 CTTCGCCTTGTACTTGCTGTCGACGCGACTGCCCGCGGGCGAGACTGGCTCACCGAGG
 AGGCTGGAGGCAGGTGCGCTGTGGTCCCCCTCGACCTGGCAGAGCTGCGGGAGCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTGCTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTGCCATCCCCGGCTCCAGCTCCTGAATGTTTAGCTGGTGCCT
 TGTTGGGCCATGGCTGGGCTCTGCTGTGTTGACCTCGGTGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTGGCAAACAGTTGGTGGTGCCTACTTCCTGATAAAGT
 GCCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTGTTTTCTATTGTTT
 TGAGACTTTCCCCATGACACCAAACGGTTCTGAAACCTCTCGGCCCAATTCTGAACATT
 CCCATCGTGCAGTTCTCTCAGTTCTATGGTTGATCCCATAATTCTGTGT
 GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTGGATGCTCTTCTCCTGGACACTG
 TCTTAAGCTGTTGCCATTGCCATGGTGGCATTAATTCTGGAACCCCTCATTAaaaaATT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATACACAGTAGAAAAGA
 CACA**TGA**CTGGATTTCTGTTGCCACATCCCTGGACTCAGTGCTTGTGTAATGGA
 TGTGGCCTCTAAAGCCCTCATTGTTGATTGCCCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTCAGAAAGGACACTCTGCTCTGAAAGGTGATTACATCAGGT
 TTTCAAACCAGCCCTGGTAGCAGACACTGCAACAGATGCCCTAGAAAATGCTGTTGT
 GGCGGGCGCGGTGGCTCACGCCGTAAATCCAGCAGCTTGGGAGGCCAGGCCGGTGATTC
 ACAAGGTCAAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAATCCTGCTCTAATAAAAAT
 ACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPRGRRLGSTEEAGGRSLWFPSDLAELRELSEVLREYR
KEHQAYVFLLFCGAYLYKQGFAIPGSSFLNVLAGALFGPWLGLLLCCVLTSGATCCYLLSS
IFGKQLVVSYFPDKVALLQRKVEENRNSLFFFLLFLRFPMTPNWFLNLSAPILNIPIVQFF
FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVKLLAIAMVALIPGTLIKKFSQKHLQ
LNETSTANHIHSRKDT

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCCGAGGGGGCGCGAGCCCCGATGAATCATTGTAGTCAATCATT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTCCGAACTGCCAGCTCAGAA
 TAGGAAAATAACTGGGATTTATATTGGAAGAC**ATG**GATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAAACTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTATCAGACAGCTGCTGGAAAAGAAATGAACCTCAGAGACC
 CCCCCCGCAGTATCCTCTCCTTATAGTTGTATAAGGTTCTCGAACCTGGGATTAATCT
 TGCTCACTGCCTACTTGTGATTCAACCTTCAGCCCATTAGCACCTGAGCCAGTGCTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTGCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTCCCTCTGCATGGGGGTGATGAAGACAGACCCCTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCC
 AACTGCACTGGCTGTGCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTC
 AGCATTGGTGTGCCAGTACCCCTGAGGCGACAGAAGGCTTCTGAAGGGTTTCGCCAAG
 TGGTGGCGCTGCTTCCTGAGCGGTGGTCCCATTCCATTCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTCCCTGTTCACTCACCTGCCATTCCAAAAGATG
 CCTCTTAAACAAGTGCTCCTTCTCACCCAGAACCTGTTGGGGAGTAAGATGCATAAG
 ATGCCTGACCTATTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTCCA
 GTGCCGAAGACATTGTCAGTCTGTGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCACCCACTGGAAGGTCTACGTTAGCCAGAGGGGTCCAGCCTTGGTCACTGCGAT
 GGAACCGCTTCTCAGAACTG**TAG**GAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCAGGTTGAAAGGGAAAAATAAAACAAAAACGATGAAACTGCAAAA

FIGURE 20

MDLAANEISIYDKLSETVDLVRQTHQCGMSEKAIEKFIRQLLEKNEPQRPPPQYPLLIVVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSЛИHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRPFDPFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFPPYPWRRPLNRSQMLRELFPV
FTHLPFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCQSVAMP
IEPGDIGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

FIGURE 21

CCACGGTGTCCGTTCTCGCCCCGGCGGCAGCTGTCCCCGAGGCAGGGAGGAGCCCGAGGGCG
CGAGCCCCGCATGAATCATTGTAGTCATCAATCATTCCAGTTCTCAGCCGTTCAGTTGTGATC
AAGGGACACGTGGTTCCGAACTGCCAGCTCAGAATAGGAAAATAACTGGGATTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTATGACAAACTTCAGAGACTGTTG
ATTTGGTGAGACAGACGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTATC
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGAACCTGGGATTAATCTTGCTCACTGCCTACTTGTGATTCAAC
CTTCAGCCCATTAGCACCTGAGCCAGTGCTTGTGGAGCTCAC

FIGURE 22

CCCACGCGTCCGCCACCGTCCGGCTGAACACCTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCTGGCTGGTG
 CCACTGGTGCACGCTGCTAGACCGTGCCTATGAGCCGCTGGGCTGAGTGGGACTGCC
 CTCCCTGCCACCCACCAATGGCAGCCCCACCTCTTGAAGACTTCCAGGCTTTGTGCCA
 CACCCGAATGGCGCCACTTCATGACAAACAGGTACAGCCAACC**ATG**TCCAGTTCGAAATG
 GACACGTATGCTAAGAGCCACGACCTTATGTCAGGTTCTGGAATGCCCTGCTATGACATGCT
 TATGAGCAGTGGGCAGCGGGCAGTGGGAGCGCGCCAGAGTCGTCGGGCCTCCAGGAGC
 TGGTGCCTGGAACCTGCGCAGAGGGGGCGCCCTGGAGGGCTACGCTACACGGCAGTGCTG
 AAGCAGCAGGCAACGAGCACTCCATGCCCTGCTGACTGGGGGGCGTGTGGCGCCAGCT
 CGCCAGCCCATGTGGGCCCTGGCGCTGAGGGACACTCCCATCCCCGCTGGAACACTGTC
 GCGCCGAGACATATTACCGCATGCCCTGAAAGCTGGGTGAGGTTCCCTGACACCCACCGAGGAGC
 CTGGAAGCCAGCGCTCTCCGAGACAATCTGGGTGAGGTTCCCTGACACCCACCGAGGAGC
 CTCACTGCCTCTGGCAGTGACCAAAGAGGCCAAAGTGAGCACCCACCCGAGTTGCTGCAGG
 AGGACCAGCTCGCGAGGGACGAGCTGGCTGAGCTGGAGACCCGATGGAGGCAGCAGAACTG
 GATGAGCAGCGTGAGAAGCTGGTGTGTCGCCAGTGCTGACGGTAGTGGCGT
 GGTCCCAGGGCTGCTGGAGGTACCCACACAGAACATGTATACTTCTACGATGGCAGCACTGAGC
 GCGTGGAAACCGAGGGAGGCATCGCTATGATTCCGGCGCCACTGGCCAGCTGCGTGAG
 GTCCACCTGCGCGTTCAACCTGCGCGTTCAGCACTTGAGCTCTTCTTATGATCAGGC
 CAACTACTCCTCAACTTCCCATGCAAGGTGGCACGCCAGTCATCTCTAGCCAGA
 CTCCGAGACCCAGCCTGGCCCATCCCCATACCCAGGTACGGAACCCAGGTGTACTCG
 TGGCTCCTGCGCTCACGGCCCCCTCTCAAGGCTACCTAACGCGCTCCCCCAGGAGAT
 GCTGCGTGCCTCAGGCCTTACCCAGAAATGGGTACAGCGTAGGATATCAACTTCGAGTACT
 TGATGCAACTCAACACATTGCGGGCGGACCTACAAATGACCTGTCTCAGTACCTGTGTC
 CCCTGGGTCTGAGGACTACGTGTCCCCAACCTGGACCTCAGCAACCCAGCCGTCTTC
 GGACCTGTCTAAGCCATCGGTGTGGTGAACCCCAAGCATGCCAGCTGTGAGGGAGAAGT
 ATGAAAGCTTGAGGACCCAGCAGGGACCATTGACAAGTTCACTATGGCACCCACTACTCC
 AATGCAGCAGCGTGTGCACTACCTCATCCCGTGGAGCCCTCACCTCCCTGCACGTCCA
 GCTGCAAAGTGGCGCTTGTACTGCTCCGACCGGAGTTCCACTCGGTGGCGGCAGCCTGG
 AGGCACGCCTGGAGAGGCCCTGCCGATGTGAAGGAGGCTCATCCCGAATTCTCTACTTCT
 GACTCTGGAGAACAGAACCGGTTTGTACCTGGCTGTCTCAGCTGACCAACGAGAAGGT
 AGGCATGTGGTGTCTACCCCGTGGCCAGCTCTCTGAGGACTTACCCAGCAGCACCGCC
 AGGCTCTGGAGTCGGAGTATGTGTCTGCACACCTACAGAGTGGATCGACCTCATCTTGG
 TACAAGCAGCGGGGCCAGCCGGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCAGGAACGGAAAGGCTCTGGAGGGCATTA
 TCAGCAACTTGGGCAGACTCCCTGTCAAGTGTGAGGAGGCCACATCCAACCTGGCTCTCA
 GCTGAGGAAGCAGCCATGCCCTGCACGCCCTGGACACTAACCTACACTAGCATCTCCAGCA
 CCTGGACGAACTCAAGGCATTCTCGCAGAGGTGACTGTGAGTGCCAGTGGCTGCTGGCA
 CCCACAGCTGGTGCCTATGACCGCAACATAAGCAACTACTCAGCTCAGCAAAGACCC
 ACCATGGGCAGCCACAAGACGCAGCGACTGCTGAGTGGCCGGTGGCTGCCAGGCAGTGGT
 GAGTGGACAAGCACTGGCAGTGGCCGGATGGAAGACTGCTATTCAAGCGGTGGCCACTGG
 ATGGCAGCCTGCGGGTGAATGCACTACCCCGTGGCAAGCTGTGAGGCCAGCTCAGCTGCCAC
 CTTGATGTAGTAACCTGCCCTGCACTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCG
 GGACACCACTGTGCAGGTCTGTATGGGCATGGGCTGAGCTGAGCTGTGAGGCTGGCCAC
 CAAAGCCTGTGCAGGTCTGTATGGGCATGGGCTGAGCTGAGCTGTGAGGCTGGCCAC
 GAACCTGACATGGCTGTGTGGATCTGAGGATGGAACACTGTGATCATACACACTGTACGCC
 CGGACAGTTGTAGCGGCAACTACGCCCTGGGTGCCACATTCCCTGGACCTATTTCCACC
 TGGCATTGGGTCCGAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGGAACGTCTGGGCC
 CAGGTACACCTACTCCTGCACCTGTATTCACTGAGGAAAGTTGCGGGCTTCACTGCCCT
 GGCAGAGCAGCCTACAGCCCTGACGGTGACAGAGGACTTGTGTTGCTGGGCACCGCCAGT
 GCGCCCTGCACATCCTCAACTAAACACACTGCTCCCGGCCGCTCCCTGCCCCATGAAG
 GTGGCCATCCGCAGCGTGGCCGTGACCAAGGAGCGCAGCCACGTGCTGGTGGGCTGGAGGA
 TGGCAAGCTCATCGTGGTGTGGCAGGGCAGCCCTCTGAGGTGCGCAGCAGCCAGTTCGCG
 GGAAGCTGTGGCGGTCTCCGCCGCGCATCTCCAGGTGTCTCGGGAGAGAGCAGGAATAAAC
 CCTACTGAGGCAGCGC**TGA**ACCTGGCCAGTCCGGCTGCTCGGGCCCGCCGGCAGGCC
 GCCCGGGAGGCCGCCAGAAGTCGGCGGAACACCCCGGGGTGGGCAGCCCAGGGGGTGA
 GCGGGGCCACCCCTGCCAGCTCAGGGATTGGCGGGCATGTTACCCCTCAGGGATTGGCG
 GCGGAAAGTCCCGCCCCCTGCCGGCTGAGGGGCCGCGCTGAGGGCCAGCACTGGCGTCT

FIGURE 23

MSQFEMDTYAKSHDLMMSGFWNACYDMLMSGQRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSAETYSRMRLKLVPN
 HHFDPHLEASALRDNLGEVPLPTTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELAELET
 PMEAELDEQREKLVLSAECQLVTVVAVVPGLEVTTQNVFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRSALELFIDQANYFLNFPCKVGTPVSSPSQTPRPQPGPIPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPTLDLSNPNAVFRDLSPKPIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSAAAWQARLESPADVKE
 LIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYCTYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPTMGSHKTQRLLSGPWPVGSGVSGQALAVAPDGKLLFSGGHWDGSLRVTLPRGKLL
 SQLSCHLDVVTCLALDTCGIYLISGSRDTTCMVWRLHQGGLSVGLAPKPVQVLYGHGA
 AVSCVAISTELDMAVSGSEDGTVIHTVRRGQFVAALRPLGATFPGPIFHLALGSEGQIVVQSSA
 WERPGAQVTYSLHLYSVNGKLRASLPLAEQPTALTVDFTVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTEAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGCGGACGCGTGGGGCTGTGAGAAAGTGCAATAATACATCATGCAACCC
 CACGGCCCACCTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTCCAGGGCTACTCAT
 CCAAAGGCCTAATCCAACGTTCTGTCTCAATCTGCAAATCTATGGGTCTGGGGCTCTC
 TGGACCCTTAACGGGTACTGCCCTGGCCAATGCGTCCTCGCTGGAGCCTTGCCTCCTT
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGTCATTGGCATTGGAGCCCTACCTGACCCCTGTGCAG
 ATAGCCCAGGTACCTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCTGTAGC
 CCGCTGCATCATGTGCTTTCAAGTGCTGCCCTGGTGTCTGGAAAAATTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATGCCATCTACGGGAAGAATTCTGTGTCTAGCCAAA
 AATGCGTTCATGCTACTCATGCGAACATTGTCAGGGTGGTCGTCTGGACAAAGTCACAGA
 CCTGCTGCTGTTCTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGTCTGTCCTCTTT
 TTTCTCCGGTCGCATCCCGGGCTGGTAAAGACTTAAAGAGCCCCCACCTCAACTATTAC
 TGGCTGCCCATCATGACCTCCATCCTGGGGCTATGTCATGCCAGCGGCTTCTCAGCGT
 TTTCGGCATGTGTGGACACGCTCTCCTCTGCTTCTGGAAAGACCTGGAGCGAACACG
 GCTCCCTGGACCAGCCCTACTACATGTCCAAGAGCCTCTAAAGATTCTGGCAAGAAC
 GAGGCGCCCCCGGACAACAAGAAGAGGAAGTGACAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCCACCCCCACCGTCCAGCCATCCAACCTCACTCGCCTTACAGGTCTCCATTGTGGT
 AAAAAAAAGTTTAGGCCAGGCAGCGTGGCTACGCCGTGAATCCAACACTTGAGAGGCTG
 AGGCAGGGGGATCACCTGAGTCAGGAGTTGAGACCAGCCTGCCAACATGGTAAACCTCC
 GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTCCAGCTAC
 TCGGGAGGCTGAGGCAGGAGAACGCTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAAGATTTATTAAAGATATTGTAACTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHVNSSCPGLMCVFQGYSSKG LIQRSVFN LQIYGVLGLF
WTLNWVLALGQC VLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLA FGALIL TLVQ
IARVILEYIDHKLRGVQN PVARCIMCCFKCCLWC LEKFIKFLNRNAYIMIAI YGKNFCVSAK
NAFMLLMRNIVRVVVL DKVTDL LLFFGKLLVVGGVGVL SFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNN GSLDRPY YMSKSLLKILGKKN
EAPPDNKKRK K

FIGURE 26

GAGTCTTGACCGCCGCCGGCTCTGGTACCTCAGCGCAGCGCCAGGCCTCCGGCCGCGT
 GGCT**ATG**TTCGTGTCCGATTCCGAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGTCC
 TTCTCTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTCAAGATCCTCAGGCCTGTTC
 CAGTGTGACCACGTGCAATATACTGCTGGTCCAGTTCTGGTGGCAAGAACACTGAAACTGC
 ATTTCTTGAGCATAAAGAACAGTTCATTATTTATTCTCATAAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTGTGTGACTCCCATAAGG
 CCAGTCAATGTCGTCAATGTATAACGATAACCGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCCCGCTATGAAGACATCTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGTGGTCAGAGCCTCTGAGAACGACACGGTTAGAACAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGCGAGAGTGGAGGCCGGAGAACAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGACATCGTCAGCCATGGTGTGTTGAGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGCCATCGTGGACTAACAGAC
 CAGTGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGCAGCG
 CCACGTTCCGCCACAACCACCGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTGAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTCAAGCTGTGGTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCTGCAGACATGGTCTTCCCTGAAGCAGGTGAAGCAGAACAGTCC
 AGGCCATGGACATCTCCTGAAGGAGAATTGGGGAAATGATTGAAGAGTCTGCAAATAAA
 TTTGGGATGAAGGACATGCGCGTGCAGACTTCAGCATTCTGGGTTCAAGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTGCCACCATGTCTTGATGGAGAGCCCCGAGAACGGATGGCT
 CAGGGACAGATCACTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAACTCGCCAAGAACGAGCAGCTGCGAGGCCACCCAGCAGACCATTGCCAGCTG
 CTTTGCACCAACCTCGTCATCTCCAGGGCCTTCTGTACTGCTCTCATGGAGGGCAC
 TCCAGATGTATGCTGTTCTAGGCCGGCATCCCTAACGCTGCTCAGCAAACACCTGCTCA
 AGTCCTTGTGTTGACAAAGAACCGCGCTGCAAACGTGCTGCCCTGGTATGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGCATCCCCCAGAGAACCGACAGCTC
 GGACAGGAAGAACCTTTGGGAGGGCGTTGAGAAGGCAGCGGAAAGCACAGCTCCGGA
 TGCTGCACAACCATTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTT
 CTGGACGCACCTATTCCCTGTCC**TAG**GAATTGATTCTCCAGAATGACCTTCTTATT
 TATGTAACTGGCTTCATTAGATTGTAAGTTATGGACATGATTGAGATGTAGAACGCCATT
 TTTTATTAAATAAAATGCTTATTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVLCAACKILQALFQCDHVQYTLVPVSGWQELETAFL
LEHKEQFHYFILINCGANVDLLDILQPDDEDTIFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAYEDIFRDEEEDEEHSGNDSDGSEPKRTRLEEEIVEQTMRRQRREWEARRDILF
DYEQYEHGTSSAMVMFELAWMLS KDLNDMLWWAIVGLTDQWVQDKITQMKYVT DVGVLQRH
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHD SLCNTSYTAARFKLWSVHGQKR
LQEFLADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGS GTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHF DLSVIELKAEDRSKFL
DALISLLS

FIGURE 28

GTACCTCAGCGCGAGGCCAGGCAGCGTCCGGCCGTCGGCTATGNTCGTGTCCGATTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTCCAGTGTGACCANGTGAATATANGCT
GGTCCAGTTCTGGGTGGCAAGAACTTGAAACTGCATTCTTGAGCATAAAGAACAGTTTC
ATTATTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTAACCTGAT
GAAGACACTATATTCTTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

FIGURE 29

CAGGAACCCCTCTTTGGGCTGGGATTGGGACCCCTTCCAGTACCATTTTTCTAGTGAAC
 CACGAAGGGACGATAACCAGAAAACACCCCTCAACCCAAAGGAATAGACTACAGCCCCAATTG
 GCTGACTTTGGCTATAGAAAAAGAAAGGAACGAAAAGAGACAGTTTTGGAAAGCTAA
 GTCTTCCCTTATCGAGTCAGAAACCCCCCTTCTGAGCTATTACAGCTTTAACAAATT
 GAGTAAAGTACGCTCCGGTCAACC**ATG**GTGACAGCCGCCCTGGGTCCCGTCTGGGCAGCGCTC
 CTGCTCTTCTCCTGATGTGTGAGATCCGTATGGTGAGCTCACCTTGCACAGAGCTGTGGC
 CAGCGGGCTGCCAACGGTGTGACTCTGAGGACCCCTGGATCCTGCCATGTATCCTCAG
 CCTCTTCCCGGCCGCCCCACGCCCTGCCTGAGATCAGACCCCTACATTAATACACCAC
 CTGAAGGGTGACAAAGGGGACCCAGGGCCATGGGCCCTGCCAGGGTACATGGGCAGGGAGGG
 TCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGAGATGGGCAGCCCCG
 GCGCCCCGTGCCAGAACGCCTTCTCGCCTCTCAGTGGGCCCAAGACGCCCTGCACAGC
 GGCAGGGACTTCCAGACGCTGCTTCGAAAGGGTCTTGTGAACCTTGTGATGGGTGCTTTGA
 CATGGCGACCGGCCAGTTGCTGCTCCCCTGCGTGGCATCTACTTCTCAGCCTCAATGTGC
 ACAGCTGGAATTACAAGGAGACGTACGTGACATTATGCATAACCAGAAAGAGGCTGTAC
 CTGTACGCGCAGGCCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGACCGCGTCTGGGTGCGGCTCTCAAGGCCAGCGCGAGAACGCCATCACAGCA
 ACGACTTCGACACCTACATCACCTCAGCGCCACCTCATCAAGGCCAGGGACGACT**TGA**GGG
 CCTCTGGGCCACCCCTCCCGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAG
 TTTGCACTGCTGTGAAGCAGGAAGGCCAGGGAGGTCCCCGGGACCTGGCATTCTGGGGAGA
 CCCTGCTCTATCTGGCTGCCATCATCCCTCCCAGCCTATTCTGCTCCTCTCTCT
 TGACCTATTAAAGAGCTTGTCTAACCTAAATATTCTAGAACATTCCCAGCCTCGTAGCCC
 AGCACTTCTCAAACATTGGAAATGCGATCGCAATCACCCGGGTCGTGTTAAATGCGAGATTCT
 GACTCAGCAGGTCTGAGTGGGTCCAGGATTCTGTGTTCTCATATGTTCTGGGTGATGCTG
 ATGGGGTCAGTCTATGAACCACACTGGAGCAACCAGGTTCTAGGACTTCTCAATATTCTAG
 TACTTCTGAACATTCTGGAATCCTCCCCACATTCTAGAATTCTCCACATTTTTTCT
 TGAGACAGAGTCTGCTCTGGCCAGGCTAGAGTGCAGTGGTGCATCTCAGTTCACTGC
 AACCTCTGCCCTCCGGTTCAAGCGATTCTCTGCCCTAGCCTCCCTAGTGGCTGGGATTAC
 AGGCGCTGCTACCATGCCCTGGCTAATTGGTATTGGTAGAGATGGGTTTACCA
 TTGGCCAGGGCTGGTCTGAACTCCTGACTTCAGGTGACCCACCCGCCTGGCCTCTCAAAT
 GCTGGGATTACAGGTGTGAGCCACCGTGCCTGGCAATTCCAACATTCTAAATCTCTCAT
 CCCTCCAGGGCTCCCGTCTATTGTCCTTACCCCTCCCCCTTCTTGTCTCAGGCC
 TGCAACACTGCAGCCACCGTTCATTTATTCAATTAAACACTGAGCACTCAGTGTGCT
 GGGTCCCAGGGAAAGGGTGAGGGGGTCAGACACAGGCCCTGCCCTCAGTGA
 GTCCAGCCCAGGGGGAGAGATGTGTACATAGGTTAAAGCAGACCCAGAGCTCATGGGG
 GCCTGTGTTCTGGGTGTTAGGTGCTGCTGGTCCATTACCCACTGCTCCCCAAGGCTGG
 TGGGACGGGGTCCGGTGGCAGGGCAGGTATCTCCTCCGTTCTCATCCACCTGCCAG
 TGCTCATCGTTACAGCAAACCCAGGGGCTTGGCCAGGTCAAGGGTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGCATTGGGGGGTGAAGTGGCCCCGAAGAAATGGAACCCACACCA
 TAGCTCTCCCCACAGCTGATACGGCATCCTGCGAGAAAGACCTGCCCTCCTCACTGGGATCCC
 CTTCTGCCCTCTCCAGGGCTCTGCCAGGCCCTTGCTCAGTCCCTTCACCAAGTCATCT
 GAACATTCCGTTCTCCCCAGGGCCTCCAGCTGCCCTCAGACACTGATGTCTGCCCCAGGTGCT
 CTCTGCCCTCATGCCCTCATGCCCTCAGGGGGCAGTGCCTCAGACTCCAGGCTTATCAAGGTG
 CTAAGGCCGGTGGCAGCTCCTCGTCTCAGAGGCCCTCCTCCGGCTGGTGTGCTGCC
 AAACACCTGCAGGAGAAGGGCACGGAAGCCCCAGGCTTAGAGCCCTCAGCAGGTCTGGGG
 AGCTAGAGCAAAGGAGGGACCTCAGGCCCTCCGTTCTTCTCCAGGGTGGGGTGGCCTGG
 GTTCCCCTAGCCTCAAACCCAGGTGGCCTGCCCTCTCCCCAGAGGGAGGGCAGGCC
 CCATTGGTGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCTGGGGGGTGTCTGTGCTCAC
 AGCCGAGGGAGCCGTGGCTCCATGCCAGATGACGAAACAGGGTCTGACCAAGTGC
 AGACACTGTGCTATAAACCAACCCCTGCCATGCCAGATGACGAAACAGGGTCTGAC
 GTCCAGCATGATTAAGAATGCTGTCTCCTTGGAAAAAAAAAAAAAA

FIGURE 30

MVTAALGPVWAALLFLLMCEIRMVELTDFRAVASGCQRCCDSEDPLDPAHVSSASSSGRPH
ALPEIRPYINITILKGDKDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSERSIMQSQSVMMLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

C1q domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTCGGGCCCGACCCGCCAGGAAGACT
AGGCCGCGCCTGCCCGCCGGCTCCCTGCGCCGCCCTCCGGGACAGAAGATGTG
CTCCAGGGTCCCTGCTGCTGCCGCTGCTCTGCTACTGGCCCTGGGGCTGGGTGCAGG
GCTGCCCATCCGGCTGCCAGTGCAGCCAGCACAGACAGTCTTCTGCACTGCCGCCAGGG
ACCACGGTGCCCCGAGACGTGCCACCGACACGGTGGGCTGTACGTCTTGAGAACGGCAT
CACCATGCTGACGCAGGCAGCTTGCCGGCTGCCGGGCTGCAGCTCCTGGACCTGTCAC
AGAACCCAGATGCCAGCCTGCCAGCGGGTCTTCCAGCCACTGCCAACCTCAGCAAACCTG
GACCTGACGGCCAACAGGCTGCATGAAATACCAATGAGACCTCCGTGCCCTGCCGCCT
CGAGCGCCTTACCTGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTGACACGC
TCGACCGCCTCTGGAGCTCAAGCTGCAGGACAACGAGCTGCCGGCACTGCCCGCTGCC
CTGCCCGCCTGCTGCTGGACCTCAGCCACAACAGCCTCTGGCCCTGGAGGCCGCAT
CCTGGACACTGCCAACGTGGAGGCCTGCCGCTGGCTGGTCTGGGCTGCAGCAGCTGGACG
AGGGGCTCTTACCGCCTGCCAACCTCACGACCTGGATGTGTCGACAACCAGCTGGAG
CGAGTGCCACCTGTGATCGAGGCCTCCGGGCTGACGCCCTGCCGCTGCCCTGCAGGAGCTGGATG
TGAGCAACCTAACGCTGCCAGGCCCTGCCCTGGCGACCTCTGGGCTCTTCCCCGCTGCC
CTGCTGGCAGCTGCCGCAACCCCTCAACTGCGTGTGCCCTGAGCTGGTTGGCCCTG
GGTGCAGAGAGCCACGTCACACTGCCAGCCCTGAGGAGACGCCACTTCCCGCCCA
AGAACGCTGCCGGCTGCTCTGGAGCTTGAACAGCCGACTTGGCTGCCAACGCCACACC
ACCACAGCCACAGTGCCACCAACGAGGCCGTGGCGGGAGCCCACAGCCTGTCTTAG
CTTGGCTCCTACCTGGCTTAGCCCCACAGGCCGGCACTGAGGCCCTGCCACCGTCCACCTGCC
CTGCCAACCGACTGTAGGGCCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCC
AATGGGGCACATGCCACCTGGGACACGGCACCACCTGGGTGCTGTGCCCGAAGGCTT
CACGGGCCTGTACTGTGAGAGCCAGATGGGACAGGGCACGCCCTACACCAGTCA
CGCCGAGGCCACACGGCCCTGACCTGGCATCGAGCCGTGAGCCCCACCTCCCTGCC
GTGGGCTGCAGCGTACCTCACGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA
TCGCAACCTATCGGCCCTGATAAGCGGCTGGTGACGCTGCCACTGCCCGCTCGCTG
AGTACACGGTACCCAGCTGCCAACGCCACTTACTCCGTCTGTGTCATGCCCTTGGG
CCCCGGGGGTGCCGGAGGGCGAGGAGGCCCTGCCGGGAGGCCATACACCCCCAGCCGCTCA
CTCCAACCACGCCCAAGTCACCCAGGCCCGAGGGCAACCTGCCCTCCTCATTGCC
CCCTGCCCGCGGTGCTCTGGCCCGCTGGCTGCCGTGGGAGGCCCTACTGTGTCGCC
GGCGGGCCATGGCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGCC
GGAACCTGGAGGGAGTGAAGGTCCCCCTGGAGCCAGGCCAGGGCAAGGCAACAGAGGGCGGTGGAG
AGGCCCTGCCCAAGCGGTCTGAGTGTGAGGTGCCACTCATGGCTTCCAGGGCTGCC
CAGTCACCCCTCCACGCAAAGCCCTACATCTAAAGCCAGAGAGAGACAGGGCAGCTGGGCC
GGCTCTCAGCCAGTGAGATGCCAGCCCCCTGCTGCCACACCACGTAAGTCTCAGTCC
CAACCTCGGGGATGTGTCAGACAGGGCTGTGACGACTGGCCCTGTCCCTGCC
CCTCGGTCTCCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGCCCCAGAAC
CGAGTGCCTATGAGGACAGTGTGCCCTGCCCTCGCAACGTGCAGTCCCTGGCACGGCG
GGCCCTGCCATGTGCTGGTAACGCATGCCCTGGCTCTGGCTTCCCACTGCCAGGGGA
CCCTGGGGGCCAGTGAAGGAAGCTCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGTG
TGACTCTAGTCTTGGCCCCAGGAAGGAACAAAAGAAACTGGAAAGGAAGATGCTTAA
GGAACATGTTGCTTTTAAATATATATTTATAAGAGATCCTTCCATTATTCTG
GGAAGATGTTTCAAACCTCAGAGACAAGGACTTGGTTTGTAAGACAAACGATGATATG
AAGGCCCTTGTAAAGAAAAATAAAAGATGAAGTGTGAAA

FIGURE 32

MCSRVPLLLPLLLLLALGPGVQGCPSCGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFEN
GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANLHEITNETFRGLR
RLERLYLGKNRIRHIQPGAFDTLDRLLELKIQDNELRALPPLRLPRLLLLDLSHNSLLALEP
GILDGTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAG
NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFG
PWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPPPSTAPPTVGVPVQPQDCPPSTCLNGGTCHLGTRHHLACLCPE
GFTGLYCESQMGQGTRPSPTPVTPRPPRSLTGLIEPVSPSLRVGLQRYLQGSSVQLRSRL
TYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPA
VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAQDKQVGPGAG
PLELEGVKVPLEPGPKATEGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

FIGURE 33

GAATCATCCACGCACCTGCAAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTGGCTCAT
 CTTCATCATTACATATGAGGAAATAAGTGGTAAAATCCTGGAATAACA**ATG**GAGACTCATCAG
 AAACATTACATATTTGTAGTATTGTTATGACAGCAGAGGGTGTGCTCCAGAGCTGCCAG
 AAGAAAGGAACTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGAGACTTG
 ACCCCAGGCCAACGACACTGGATTATCCTATAACCTCCTTTCAACTCCAGAGTTAGA
 TTTCATTCCTGCTCCAAACTGAGAGTTGATTCTATGCCATAACAGAATTCAACAGCTGG
 ATCTCAAACCTTGAATTCAACAAGGAGTTAAGATATTAGATTGTCTAATAACAGACTG
 AAGAGTGTAACTTGGTATTACTGGCAGGTCTCAGGTATTAGATCTTCTTTAATGACCT
 TGACACCAGCCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTGA
 GTGGGGCAAAATACAAAATCAGATTCCAGAAAATTGCTCATCTGCATCTAAACACAGCTGG
 TTCTTAGGATTCAAAACTCTCCTATTATGAAGAAGGTAGGCTGCCATCTAAACACAAAC
 AAAACTGCACATTGTTTACCAATGGACACAAATTCTGGGTTCTTTCGCTGATGGAATCA
 AGACTTCAAAATATTAGAAATGACAAATATAGATGGCAAAAGCCAATTGTAAAGTTATGAA
 ATGCAACGAAATCTTAGTTAGAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA
 TTTACTCTGGGACGACCTTCCTTATCTTACAATTGTTGGCATACTCAGTGGAAACACT
 TTCAGATCCGAAATGTGACTTGGTGGTAAGGCTTATCTGACCACAAATTGACTAC
 TCAAATACTGTAATGAGAACTATAAAATTGGAGCATGTACATTCAAGAGTGTACATTCA
 ACAGGATAAAATCTATTGCTTTGACCAAAATGGACATAGAAAACCTGACAATATCAAATG
 CACAAATGCCACACATGCTTCCCGAATTATCCTACGAAATTCCAATATTAAATTGCCC
 AATAATATCTAACAGACGAGTGTGTTAAAAGAAACTATCCAACACTGCCTACTTGAACAAACTCT
 CATTGAAATGGCAAAACTGGAGACACTTCTTGTAGTTAGTGTCTGCTAACACAC
 CCTTGGAACACTTGGATCTGAGTCAAAATCTTACAACATAAAATGATGAAAATTGCTCA
 TGGCCAGAAACTGTGGTCAATATGAATCTGTCATAACAATAATTGCTGATTCTGCTTCAG
 GTGCTTGCCTAAAGTATTCAAATACTTGACCTAAATAACCAAACTGTACCTA
 AAGAGACTATTCACTGATGGCCTACGAGAACTAAATATTGCTATTAAATTCTAACTGAT
 CTCCCTGGATGCAGTCATTCACTGAGCTTCAGTTCTGAACATTGAAATGAACTTCATTCT
 CAGCCCACATCTGGATTTCAGAGCTGCCAGGAAGTTAAAACCTAAATGCCAGGAAAGAA
 ATCCATTCCGGTGTACCTGTGAATTAAAAAATTCTTCACTCAGCTGAAACATATTGAGGTC
 ATGATGGTGGATGGTCAGATTCAACACTGTGAATACCCCTTAAACCTAAGGGAAACTAG
 GTTAAAAGACGTTCATCTCACGAAATTATCTGCAACACAGCTGTGTTGATGTCACCATG
 TGGTTATTATGCTAGTTCTGGGTTGGCTGTGGCTTCTGCTGTCTCCACTTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCATGCAACACAAATGGCACAGGGTTAGGAAAACAACCCA
 AGAACAACTCAAGAGAAATGTCGATTCCACGCATTATTATTCATACAGTGAAACATGATTCTC
 TGTGGGTAAGAATGAATTGATCCCCAATCTAGAGAAGGAAGATGGTTCTATCTGATTG
 CTTTATGAAAGCTACTTGACCCCTGGCAAAAGCATTAGTGAACATTGAAATATTGTAAGCTTCATTGA
 GAAAAGCTATAAGTCATCTTGTGTTGTCCTCCAACTTGTCCAGAATGAGTGGTGCCTATT
 ATGAATTCTACTTGCCCCACACAACTCTTCCATGAAAATTCTGATCATATAATTCTTATC
 TTACTGGAACCCATTCCATTCTATTGCACTTCCACCAAGGTATCATAAACTGAAAGCTCTCCT
 GGAAAAAAAGCATACTTGAATGGCCAAGGATAGGCGTAAATGTGGCTTTCTGGGCAA
 ACCTTCGAGCTGCTTAAATGTTAATGTATTAGCCACAGAGAAATGTATGAACTGCAGACA
 TTCAAGAGTTAAATGAAGAGTCTCGAGGTTCTACAACTCTCTGATGAGAACAGATTGCT
ATAAAATTCCACAGTCCTGGGAAGTGGGGACACATACTGTTGGATGTACATTGATA
 CAACCTTATGATGCGAATTGACAATATTATTAATGAAACACCTTCAACAGTTATAAGG
 GCTTATGAAAAAGGTGTTCATCCCAGGATTGTTATAATCATGAAAATGTGGCCAGGTGC
 AGTGGCTCACTCTGTAATCCCAGCACTATGGGAGGCCAAGGGGGTGTGACCCACGGAGGTCAA
 GAGATGGGAGACCATCCTGGCAACATGGTGAACACCCTGTCTACTAAAAATACAAAAATT
 GCTGGGCGGTGATGGTGCACGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCG
 CTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTGCACCTCCAGCCTGGT
 GACAGAGCGAGACTCCATCTCAAAAAAGAAAAAAAAGAAAAAAAGAAAAATGGAAAACATCC
 TCATGGCCACAAATAAGGTCTAATTCAATAATTATAGTACATTAAATGTAATATAATT
 CATGCCACTAAAAGAATAAGGTAGCTGTATATTCTGGTATGGAAAAAAACATATTAAAT
 GTTATAAAACTATTAGGTTGGTGCAGGAAACTAATTGTTGGGTTTGGCATTGAAATGGCATTGAA
 ATAAAAGTGTAAAGAAATCTATACCAAGATGTAGTAACAGTGGGTTGGGCTGGGAGGTTGGA
 TTACAGGGAGCATTTGATTCTATGTTGTATTCTATAATGTTGAATTGTTAGAATGA
 ATCTGTATTCTTATAAGTAGAAAAAAATAAGATAGTTTACAGCCT

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEEREIMTNCSNMSLRKVPADLTATTLDLSYNLLFQ
LQSSDFHSVSKLRLVILCHNRIQQQLDLKTFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFTMPICEEAGNMHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFILQFWHTSVEHFQIRNTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLP
HLKTLILNGNKLETLSVSCFANNTPLEHLDLSQNLLQHKNDENCSPETVVNMNLSSYNKLS
DSVFRCLPKSIQILDNNNQIQTVPKETIHLMALRELNIAFNFLTDLPGCSHFSRSLSVLNIE
MNFILSPSLDFVQSCQEVTLNAGRNPFRCTCELKNIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVLHHELCNTALLIVTIVVIMVLGLAVAFCCLHFDPWYLRLMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSIFVLSNFVQNEWCHYEFYFAHHNLFHENSDDIIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

FIGURE 35

GGGGGGCTTCTGGCTGGCTGCTGGAACACCTGCCCTCCAAGGACGGGCGCTGGAGGGTCGCCGGAAAGG
GAGGGAAAGAAGGAAGGGCGGGGCCGGCCCCCTGCGCCGCCCTGCGGCCCTGCGGCCCTGCGGCCCTGCG
CCAGCCCAGCCCAGGGCGGGCGGTACACGCGCAGCCAGCGGCCCTCCCGGCCAAGGCGGCCGCT
CTGCTGTGCCCTGCCCTGGCCCCGGCCAGCTCTGCGGCCGAGCCGCCGGGCCGGCGCCCCGGTGACCGTG
CCCTGCCCTGGGCCGGGGGAGCAGGCAGGCATGTCCCAGGGCGCTACCCAGCGCTGCCCTGGTGCTC
CTGGCAGTGACCTGGCGGGGCTGGAGGCCAGGGCGAGCCCTGAGGACCTGATTATTACGGGCAGGAGAT
CTGGAGCCGGAGCCCTACTACGCGCCCGGAGCCGAGCTCGAGACCTCTCCGCCGCTGCCCTGGGGC
CCGGGGAGGAGTGGAGCGGGGCCAGGAGCCAGGCCAACAGAGGGCACCAAGGCCAACAGCTCCC
AAGAGGGAGAAGTCGGCTCCGGAGCCGCCACCAGTAACACAGCAACAAAAAGTTAGAGAACCAAGAG
CTCTGAGAAGGCTGCAACGATGATCACAGTGTCCGTGTGGCCGTGAAGATGTCAGAGAGAGTTGCCAACCTC
TTGGCTGAAACCTAAAAATCACAGACTTCCAGCTCCATGCCCTCACGGTGAAGCGTATGCCCTGGGGCA
CATCGAGGGAGACTCAACATCCAGCGGGCATTATGAAAATGATTTATGACGAGCGTGTGCGCGGAAAG
AAATGACCTCCAGCAGTGGATTGAAAGTGGATGCTGGCGCTGACCAGATTCACTGGTGTATCACTCAAGGGA
GGAACCTCCCTGCTGAGTGACTGGGTGACATCTATAAGGTATGGTAGCAATGACAGCACAGCTGGGTG
ACTGTTAAGAATGGATCTGGAGACATGATATTGAGGGAAACAGTGAGAAGGGAGATCCCTGTTCTCAATGAGCT
ACCCGTCCCCCTGGTGGCCGCTACATCCGATAAACCTCAGTCCTGGTTGATAATGGGAGCATCTGATGA
GAATGGAGATCTGGCTGCCACTGCCAGATCCATAATTATTATCACCGCCGGAAGAGATGACCAACACT
GATGACCTGGATTAAAGCACCACAATTATAAGGAAATGCCAGTTGATGAAAGTTGTAATGAAATGTTGTC
CAATATCACCAGAAATTACACATTGGAAAAAGCCACCCAGGGCTGAAAGCTGTTGAGATCTCAGATC
ACCCCTGGGAGCATGAAAGTCGGTGGCCGACTACATCGCGGGGGGCCACGGCAATGAGGTGCTGGC
CGGGACCTGCTGCTGCTGGTGGCAGTTCTGTCAGGAGTACTTGGCCCGGATGCCGCATGTCACCT
GGTGGAGGAGACCGGATTACGTCCTCCCTCCCTGAAACCCGATGGCTACGAGAAGGCCTACGAGAAGGGGCT
CGGAGCTGGAGGCTGGTCCCTGGGACGCTGGACCCACGATGGAATTGACATCAACAAACATTCTGATTAA
AACACGCTGCTGGAGGAGCAGAGGATGACAGAATGTCCTCAGGAAAGTTCCCAACTACTATATTGCA
TGAGTGGTTCTGCGAAATGCCACGGTGGCTGCCAGACAGAGTCATAGCCTGGATGAAAGAAATCC
CTTTGTGCTGGCGCAACCTGCAAGGGCGCGAGCTGGTGGCTATCCCTACGACCTGGTGCCTGGGG
TGGAAAGACGCAAGAACACACCCCCACCCCCGATGACCACGTGTTCCGCTGGCTGGCTACTCTATGCCCT
ACACCGCTCATGACAGACGCCGGAGGGAGGTGTGCCACACGGAGGACTCCAGAAGGAGGGCACTGTCA
ATGGGGCTCCTGCCACACCGTCGCTGAAAGTCTGAAACGATTCACTACCTCATACAAACTGCTTCGA
TCCATCTACGTCGGCTGTGATAAAATACCCACATGAGAGGCCAGCTGCCAGGGAGTGGGAGAAATACCGGA
TCTGATCGTGTTCATGGAGCAGGTTACGTCGCTTAAAGGCTTGGTGGAGGATTACATGAAAAGGA
CAAACGCCATTATCTCCGTTAGAAGGCATTAACCATGACATCCGAACAGCAACGATGGGATTACTGCC
CTGAACCTGGAGAGTATGTGGTACAGCAAAGGCCAGGGTTACTGCATCCACCAAGAACACTGATGGT
CTATGACATGGGGCCACAAGGTGTGACTTACACTTAGAAAACACATGCCAGGATCCAGAGAGATCATGG
AGAAGTTGGGAAGCAGCCGTCAGCCTGCCAGGCCAGGTGAAGCTGCCGGGGCGGAAGAGACGACAGCGT
GGG**TG**ACCCCTCTGGCCCTTGAGACTCGTCTGGACCCATGCAAATTAAACCAACCTGGTAGTGC
TGGACTCACTGTTGTTCTCTGTAATTCAAGAAGTGCCTGGAGAGAGGGTGCATTGTGAGGAGCG
CAAAGGGAAAGGCTGGAGGCTGAGGTGTTCTTCTTCTTCTGCTCCATTATCCAAATAACTGGACAGAGCA
GCAGAGAAAAGCTGATGGGAGTGGAGAGAACTCAGCAAGCCACCTGGGAATCAGAGAGAGAAGGAGGG
GAGCCTGTCGTTAGAGCCTCTGGCTGATAGAAAAGGATTCTGGTGTCTCCCTGTTGGCTGCCAGCA
GTTCCACGTCATTGCAATTGACAGCTAAATTGACGCTTCCCGAGCTGGCTGTCCTAAATGTACCA
TTTGAGATGCTCCACGGCTCTAAGGAAATCACCCTCTGGGCTGGGAGCATGCAAGCTGCTACAAATAA
ATTCTGTTCTTGTGACAATAGCGTCAATTGCCAAGTGCACATCAGTGAGCCTCTGTAATCTGTTAGTCT
TTTCAACAAAGGAGTGTGTTAGAAAAGGAGAGAGAGGGCTGAGATCATTGAGGATTGTTGGCAGCA
TGGAGCTTCTGCAAAATTCTGGGTCATAAACACCCCCAAAGTCCCTGCTGATCCAGTGCAGCTGGAGGTT
CCCCAGGTAGGGAGAGCCAGGGTGCCTGCCAGGCCAGGGTGAAGGCCAGAAAATTGAGCTGGATCT
CTGCTAGGACTGGAAAGAGCCAGAAGTGGGGTGGCTGAAGCCCTCTCTGCTTGGAGGTTATTGCC
GAATTGAGTGCATGGGTTGGCCTCATATCAGCCTGGAGTTATTGATATGAGAATGCCAGATCTTCCA
GATTAGGCTAAATGTAATGAAAACCTCTAGGATTATCTGTTGGAGCATCAGTTGGGAAGAATTATTG
CTTGCAAGAAAAAGTATGTCCTACATTGTTAATGTTGCTGCCATTGACCTGGAAAATGAAAAAA
AATGACAAATGTTAAGACCCCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGAALEDPDYYGQEWSREPYYARPEPELETFSPP
AGPGEWERRPQEPRPKRATPKKAPKREKSAPPEPPPGKHSNKKVMRTKSSEKAANDH
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPMVARYIRINPQSFDNGSICMRMEILGCPLPDPNNYYHRRNEMTT
TDDDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHGEHEVGEPEF
HYIAGAHGNEVLGRELLLLVQFVCQEYLARNARIHLVEETRIHVLP SLNPDGYEKAYEGG
SELGGWSLGRWTHDGINNNFPDLNTLLWEAEDRNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAMEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSYAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGIPNAIIISVEGINHDIRTANDGDYWRL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTLSKTNMARIREIMEKFGKQPVSLPARR
LKLRGRKRRQRG

FIGURE 37

CTAAGAGGACAAG**ATG**AGGCCGGCCTCTCATTTCTCTAGCCCTCTGTTCTTCCTGGCCAAGCTGCAGGGG
 ATTTGGGGATGTGGACCTCCAATTCCCAGCCCCGGCTCAGCTCTTCCCAGGTGTTGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGGTGGGCTCCAGCTCCAGCCGAGCTTAGGCAGGGAGGTTCTGTGTCAGTTGTT
 TTCCAATTCAACCGGCTCCGTGGATGACCCTGGACCTGCCAGTGCTCTGTTCCCTGCCAGACACCACCTTC
 CGTGGACAGAGTGGAACGCTTGAATTCACAGCTCATGTTCTTCAGAAGTTGAGAAAGAACCTTCTAAA
 GTGAGGAATATGTCCAATTAAATTAGTGTGTTGAAAAGAAACTGTTAAACCTAAGTGTCCGAATTGACATCAT
 GGAGAAGGATAACCTTACACTGAACCTGGACTTCGAGCTGATCAAGGTAGAAGTGAAGGAGATGGAAAAAC
 TGGTCATACAGCTGAAGGAGAGTTGGTGGAGCTCAGAAATTGTTGACCAGCTGGAGGTGGAGATAAGAAAT
 ATGACTCTTGGTAGAGAAGCTTGAGACACTAGACAAAACAATGTCCTGCCATTGCCAGAGAAATCGTGGC
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCTCTAAAGATCAAACACCCCTGTCGTCACCCTCCACTC
 CAGGGAGCTGTGGTCAATGGTGGTGGTGAACATCAGCAAACCGCTGTCGTTCAAGCTCAACTGGAGAGGGTT
 TCTTATCTATGGTCTGGGAGTTACTCTCCCAGCATCCAAACAAAGGACTGTATTGGTGGCGCC
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAAACACACTGGATGATTGCTATTGTATATAA
 ATGCTCGAGAGTTGGGATCACCTATGCCAAGGTTAACCTGACCCACAGCTGACTCAAACATGTACGTCAAC
 ATGTACAACACCGGAATATTGCCAAGGTTAACCTGACCCACAGCTGACTCAAACATCTCCCTAA
 TGCTGCCTATAATAACCGCTTTCATATGCTAATGTTGCTGGCAAGATATTGACTTGTGGATGAGAATG
 GATTGTGGTTATTATTCAGACTGAAAGCCACACTGGTAAACATGGTATTAGTAAACTCAATGACACCACATT
 CAGGTGCTAAACACTGGTATACCAAGCAGTATAAACCATCTGTTCTAACGCCCTCATGGTATGTGGGTTCT
 GTATGCCACCGTACTATGAACACCAAGAAGAGATTTTACTATTATGACACAAACACAGGGAAAGAGG
 GCAAACATAGACATTGTAATGCATAAGATGCAGGAAAAGTGCAGAGCATTAACTATAACCCTTGACCAGAAA
 CTTTATGCTATAACGATGGTACCTCTGAATTATGATCTTCTGCTTGAGAAGCCCCAG**TAA**GCTGTTA
 GGAGTTAGGGTAAAGAGAAAATGTTGTTGAAAAAATAGTCTCTCCACTTACTTAGATATCTGCAGGGGTGT
 CTAAAAGTGTGTCATTTGCAGCAATGTTAGGTGCATAGTTCTACCACACTAGAGATCTAGGACATTGTCT
 TGATTGGTGAGTCTCTGGGAATCATCTGCCTCTCAGGCCTATTGCAATAAGTGTCTAGGGTGGGA
 TTGTCAGAGGTCTAGGGCACTGTGGCCTAGTGAAGCCTACTGTGAGGGCTCACTAGAACGCTTAAATTA
 GGAATTAAAGGAACTTAAACTCAGTATGGCTCTAGGGATTCTTGACAGGAATATTGCCAATGACTAGTC
 CTCATCCATGTAGCACCCTAAATTCTCATGCCCTGAAAGAACCTGGGACTTAGTTAGGTAGATTAATATCT
 GGAGCTCCCTGAGGGACCAATCTCAAACCTTTTCCCTCACTAGCACCTGGAATGATGCTTTGTATGTGG
 CAGATAAGTAAATTGGCATGCTTATATATTCTACATCTGTAAGTGTGAGTTTATGGAGAGAGGCCTTTT
 ATGCAATTAAATTGTACATGGCAATAAAATCCCAGAAGGATCTGTAGATGAGGCACCTGCTTTCTTTCTC
 ATTGTCCACCTTACTAAAGTCAGTAGAATCTCTACCTCATAACTCCTCCAAAGGCAGCTCAGAACGATTAG
 AACCAACACTAAACCAATTCCACCCCCCACCACCCCTCTACTGCCTACTTTAAATTAATAGTTT
 CTATGGAACGTCAAGATTAGAAAAAATTAATTCTTAAATTCTCATTAGGACTTTTACATGACTCTA
 AGACTATAAGAAAATCTGATGCCAGTGACAAAGTGTCTAGCATTTATTGTTATCTAATAAGACCTGGAGCATA
 TGTGCAACTTATGAGTGTATCAGTTGTTGCTGATGTAATTTCCTGTTAAGCCTGGAACCTGTAAGAAAAT
 GAAAATTAAATTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAGTAGT
 TGGAAACCTTGTGGTATGTGATGTGCTCTGTGCTTTGAATGACTTATCATCTAGTCTTGTCTATT
 CCCTTGATGTTCAAGTCCTAGTCTATAGGATTGGCAGTTAAATGCTTACTCCCCCTTTAAATAAATGAT
 TAAAATGTGCTTGAAAAA

FIGURE 38

MRPGLSFLLALLFFLGQAAGDLGVGPPIPSFGSSFPGVDSFFFSSSRSGSSSRSLGS
GGSVSQLFSNFTGSVDDRGTCQCSVSLPDFFPVDRVERLETAHVLSQKFEKELSKVREYV
QLISVYEKLLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSQHPNKGLYWVAPLNTDGRLEYYRLYNTLD
DLLLYINARELRITYGQGSGTAVYNNMYVNMYNTGNIARVNLTNTIAVTQTLPNAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTLQVLNTWYTKQYKPSASNAF
MVCGVLYATRTMNTRTEEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPQ

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACCTCCAGGGAGCTGTGGTATGGTGGTGGTGAACATCAGCAAACCGTCTGT
GGTCAGCTCAACTGGAGAGGGTTTCTTATCTATGGTCTGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTGCTATTGTATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTACAACAACATGTACGTCAACA
TGTACAACACCGGGNATATTGCCAGAGTTAACCTGACC

FIGURE 40

TCTCGCAGATAGTAAATAATCTCGAAAGGCAGAAAGAAGCTGTCTCATCTTGTCTGTAT
 CCGCTGCTCTTGTGACGTTGGAG**ATG**GGGAGCGCTCTGGGCTGTGCTCCATGGCGAGCT
 GGATACCATGTTGTGGAAGTGCCCGTGTGCTATGCCATGCTGTCTAGTGGAAAC
 AACTCCACTGTAACTAGATTGATCTATGCACTTTCTTGTGTTGGAGTATGTGTAGCTTG
 TGTAATGTTGATACCAGGAATGGAAGAACAACTGAATAAGATCCTGGATTTGTGAGAATG
 AGAAAGGTGTTGTCCTGTAACATTGGTGGCTATAAAGCTGTATATCGTTGTGCTTT
 GTGTTGGCTATGTTCTATCTCTCTTACTAATGATCAAAGTGAAGAGTAGCAGTGA
 TCCTAGAGCTGCAGTGCAACATGGATTTGGTCTTAAATTGCTGCAGCAATTGCAATT
 TTATTGGGGCATTCTCATCCAGAAGGAACCTTTACAACAGTGTGTTGTGAGCTTGTGCT
 GCAGGTGCTCTTGTGTCATCCTCATACAACAGTCTTACTTATTGATTTGCACATTGATG
 GAATGAATCGTGGGTTGAAAAAAATGGAAGAAGGGAAACTCGAGATGTTGGTATGCAGCCTGT
 TATCAGCTACAGCTCTGAATTATCTGCTGTTAGTTGCTATCGTCTGTCTAC
 TACACTCATCCAGGCCAGTGTGTCAGAAAACAAGGCCTCATCAGTGTCAACATGCTCCTGT
 CGTGGTGCCTCTGTAATGTCATACTGCCAAAATCCAAGAATCACACCAAGATCTGGT
 TGTTACAGTCTTCAGTAATTACAGTCTACACAATGTATTGACATGGTCAGCTATGACCAAT
 GAACCAGAAACAATTGCAACCCAAGTCTACTAAGCATAATTGGCTACAATACAAAGCAC
 TGTCCCCAAGGAAGGGCAGTCAGTCCAGTGGCATGCTCAAGGAATTAGGACTAATTC
 TCTTTTGTGTTGTTGATTTTATTCCAGCATCCGTACTTCAAACAATAGTCAGGTTAATAA
 CTGACTCTAACAAAGTGTGAAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTGTGATGGATC
 ACTGGAGGATGGGGACGATGTTCACCGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACA
 GTTATTCTCTTCACTTCATGCTTCTGGCTTCACTTATATCATGATGACCTTAC
 AACTGGTCCAGGTATGACCTCTCGTGGAGATGAAAAGTCAGTGGACAGCTGTCGGTGA
 AATCTCTCAGTTGGATTGGCATCGTGTGAGATGAAAAGTCAGTGGACAGCTGTCGGTGA
 TTACAAATCGTGATTGACT**TGA**GTGAGACTCTAGCATGAAAGTCCCACTTGATTATTGC
 TTATTGAAAACAGTATTCCAACCTTTGTAAGTTGTTGATGTTGCTTCCATGTAAAC
 TTCTCCAGTGTCTGGCATGAATTAGATTGCTTGTCAATTGTTGATTTCTTACCAA
 GTGCATTGATATGTGAAGTAGAATGAATTGAGAGGAAAGTTTATGAAATATGGTGTGAGT
 TAGTAAAAGTGGCATTATTGGCTTATTCTCTGCTCTATAGTTGAAATGAAGAGTAAA
 ACAAAATTGTTGACTATTAAAATTATATTAGACCTTAAGCTGTTAGCAAGCATTAA
 GCAAATGTATGGCTGCCTTGTGAAATATTGATGTGTTGCCTGGCAGGATACTGCAAAGAAC
 ATGGTTATTAAAATTAAACAAGTCACCTAAATGCCAGTTGTCGAAAATCTTATA
 AGGTTTACCCCTGATACCGAATTACACAGGTAGGGAGTGTGTTAGTGGACAAATAGTGTAGG
 TTATGGATGGAGGGTGTGGTACTAAATTGAATAACGAGTAATATCTACTTGGTAGAGA
 TGGCCTTGCACAAAGTGAACTGTTGGTTGTTAAACTCATGAGTATGGTTCACT
 GGAAATGTTGGAACCTGAAAGGATTAGACAAGGTTGAAAAGGATAATCATGGTTAGA
 AGGAAGTGTGTTGAAAGTCACCTTGAAAGTTAGTTGGCCAGCACGGTAGCTCACCC
 GGTAAATCCCAGCACTTGGGAGCTTAAGTGGTAGATTACTGAGGCCAGGAATCAGACCA
 GCTTGGCACATGGTGAACCTGTTCTATAAAAATACTGGCTTGGCATATGCCTGTGGTC
 CAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCCAGAGCCAAGGTTGCACTGAGCAAGTCA
 CGTCACTGCACTAGCTGGCACAGAGTAAGCCAAAAAATATATATATTGAAATCAAGG
 AGGCAAAATTGACAGGGAAAGGAAGTAACGCAAAACCACTAGGCTTAGTAGGTACTTAT
 ATAAAATCTAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTAAATA
 GCTCAGATAGCTAATTAGGAAATTCAAGTGGCAATAATGACATTCTCTGACATTAA
 AAATAATTCTATTCAAAATACATGCAATTGATTTACACCTCATACTGTGATAATTAAATGT
 GATGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTAGAGAATGATGGAAATGTTT
 AGAATAAAACTCCTGCTTATAGTATACTACACAGTTCAAAGATGTTAAAATGCTTTGTAT
 TTACTGCCATGTAATTGAAATATAGATTATTGTAACCTTCAACCTGAAAATCAAGCAGT
 ATGAGAGTTAGTTATTGTATGTGCACTAGTGTCAATGAGCTTTAAAATCTACAATT
 TCTTCTTAAAAATATTATTAAATGTGAATGGAATATAACAATTGAGCTTAATTCCCCAAC
 TTATTCTGTGTGAGACATTGATTCACAAATTGAAATGGCTGTGTTACCTCTAAATAA
 ATGAATTCAAGAGAAAAAAA

FIGURE 41

MGSVLGLCSMASWIPICLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCACVMLIPGME
EQLNKIPGFCENEKGVVPCNILVGYKAVYRLCFGGLAMFYLLSLLMIKVKSSEDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFITVWFYVGGMAGAFCFILIQLVLLIDFAHWNESWVEKM
EEGNSRCWYAALLSATANLYLLSLVAIVLFFVYYTHPASCSENKAFIGVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITYTMYLTWSAMTNEPETNCNPSSLISIIGYNTTSTVPKEQGSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSL
RAVDNERDGVTVSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVWVKISSSWIGI
VLYVWTLVAPLVLNRDFD

FIGURE 42

GCGAGAAAGCTGTCCATCTTGTCTGTATCCCGCTGCTCTTGNACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTGTGGAAGTGCC
CCGTGTTGCTATGCCGATGCTGTCCTAGTGGAAACAANTCCACTGTAACTAGATTGATCTA
TGCACTTTCTTGCTTGGAGTATGTAGCTTGTGTAATGTTGATAACCAGGAATGGAAG
AACAACTGAATAAGATTCTGGATTTGTGAGAATGAGAAAGGTGTTGTCCTTGTAAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTGTGCTTGGCTATGTTCTATCTTCTTCT
CTCTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTCACAATGGAT
TTTGGTTCTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 43

GTTATTGTGAACCTTGTGGAGATGGGAGGTCNTGGGCCTGTGTTCCATGGCGAGCTGGATA
CANGTTGTGGAAGTCCCCGTGTTGNTATGCCATGCTGTCCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTNTGCTTGTGGAGTANGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACTGAATAAGATTCTGGATTTGTGAGAATGAGAAAG
GTGTTGTCCCTGTAAACATTTGGTTGGCTATAAAGCTGTATATNGTTGTGCTTGGTTG
GCTANGTTCTATNTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTGGTTTAAATTGCTGCAGCAATTGCAATTATTATTG
GGGC

FIGURE 44

AAGAACGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTAAACGTTNTGGAGATGGGGAGC
GTCCTGGGGTTGTGCTCCATGGCGAGCTGGATAACCATGTTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCCTAGTGGAAACAACCTCCACTGTAACTAGATTGATCTATGCACTT
TTCTTGCTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAACT
GAATAAGATTCCCTGGATTTGTGAGAATGAGAAAGGTGTTGTCCTGTAACATTTGGTTG
GCTATAAAGCTGTATATCGTTGTGCTTGGTTGGCTATGTTCTATCTTCTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTGGTT
CTTAAATTGCTGCAGCAATTGCAATTATTGGGGC

FIGURE 45

GCTGTCCTTAGTGGAAACAANTCCAAC TTGTAAC TGATTGATCTATGCAC TTTCCCTG
CTTGGAGTATGTGAGCTTGTAATGTTGTTCCAGGATTGGANGAACAACTGAATA
AGATTCTGGATTTGTGAGAATGAGAAAGGTGTTGCCCCTGTAACATTGGTTGGC
TATAAAGCTGTATATCGTTGTGCTTGGCTATGTTCTATCTTCTCTCTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTCACAATGGATTTGGTTCT
TTAAATTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTCATTCCAGAAGGAACCTTT
ACAACACTGTGTGGTTATGTAGGCATGGCAGGTGCCTTGTTCATCCTCATACAACTAGT
CTTACTTATTGATTTGCACATTGAAATGAATCGTGGTTGAAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTA
GTTGCTATCGTCCTGTTCTTGTCTACTACACTCATCCAGCCAGTTGTTCAGAAAACAAGGC
GTTCATCAGTGTCAACATGCTCCTGCGTTGGTGCTCTGTAATG

FIGURE 46

CTCGGGCGGCACAGGCAGCTGGTTGCCCTGCGATTGAGCTCGGGTCCGGCGCCGGCCTCCAAT
 GGAAATGTGTGGCTGGAGGGAGCGCGAGGCTTCGGCAAGGCAGTCAGTGTTGAGACCGGGCGAG
 TCCGTGAAAGCAGATAAAAGAAAACATTATTAACGTGTCATTACGAGGGAGCGCCGGCGGGGCTGTCG
 ACTCCCCGGAACATTGGCTCCCTCCAGCTCGAGAGAGAGAAGAAGAAAGCGAAAAGAGGCAGATTAC
 GTCGTTCCAGCCAAGTGGACCTGATCGATGCCCTCTGAATTATCACGATATTGATTATTAGCGATGCC
 CCCTGGTTGTGTACGCACACACAGTCACACAAGGCTCTGGCTCGTCCCTCCCTGTTCCAGCTCC
 TGGCGAATCCCACATCTGTTCAACTCTCCGCGAGGGCAGCAGGAGCAGAGTGTGTCGAATCTGCGAGTG
 AAGAGGGACGAGGGAAAAGAAACAAGCACAGACGAACCTGAGACTCCGCATCCAAAAGAACGACCAGAT
 CAGCAAAAAAGAAG**ATGG**GGCCCCCGAGCCTCGTGTGCTGCTGTCGCAACTGTGTTCTCCCTGCTGGG
 TGGAAAGCTGGCCCTTCTGTGACGCCACCGCCTGAAAGGCAGGTTCAAGAGGACCGCAGGAACATCCGCC
 ACATCATCTGGTGTGACGGACGACCAGGATGTGGAGCTGGTCCATGCAGGTGATGAACAAGACCCGGCGC
 ATCATGGAGCAGGGCGGGCGCACTTCATCAACGCCCTCGTGTGACCAACCCATGTGCTGCCCTCACGCTC
 CATCCTCAGGCAAGTACGTCACAAACACAACCTACACCAACAATGAGAACTGCTCCTCGCCCTC
 AGGCACAGCACGAGAGCCGACCTTGGCTGTACCTCAATAGCACTGGCTACCGGACAGCCTTC
 TATCTTAATGAATAACACGGCTCTACGTGCCACCCGGCTGAAGGGAGTGGGCTGGACTCCTTAAA
 ACTCCGCTTATAACTACACGGCTGTGCGGAACGGGGTGAAGAGAAGCAGGGCTCGACTACTCCA
 CAGACCTCATACCAATGACAGCGTGAGCTTCTCCGACGTCAAGAAGATGACCCGACAGGCCAGTCC
 ATGGTCATCAGCCATGCAGCCCCCACGGGCTGAGGATTCAAGCCCCACAATATTCA
 CGCCTTCCAAACGC
 ATCTCAGCACATCACGCCAGCTACAACACTACGCGCCAACCCGGACAAACACTGGATCATGCGCTACACGGG
 CCATGAAGCCATCCACATGGAATTCAACACATGCTCCAGCAGGAGCAGCTGGACACACGTACATGT
 ATACACCGC
 GACTCCATGGAGACGATTACAACATGCTGGTTGAGACGGGAGCTGGACACACGTACATGT
 ATACACCGC
 CGACCACGGTTACACATCGGCCAGTTGGCTGGTGAAGGGAAATCCATGCCATATGAGTTGACATCAGGG
 TCCCGTTCTACGTGAGGGGCCAACGTTGGAAGCCGGCTGTGAATCCCCACATGCTCCTCAACATTGACCTG
 GCCCCCCACCATCCTGGACATTGCAAGGCTGGACATACTGCGGATATGGACGGGAAATCCATC
 CAAGCTGCT
 GGACACGGAGCGGCCGTGAATCGGTTCACTTGAAAAGAAGATGAGGGCTGGCGGGACTCCTTGGTGG
 AGAGAGGCAAGCTGCTACACAAGAGACAATGACAAGGTGGACGCCAGGAGGAGAACCTTCTGCCAAGTAC
 CAGCGTGTGAAGGACCTGTGTGAGTACAGACGGCGTGTGAGCAGCTGGGACAGAAGTGGCAGTG
 TGTGGAGGACGCCAGGGGAAGCTGAAGCTGCAATAAGTGAAGGGCCCATGCGCTGGCGGGCAGCAGAGCC
 TCTCCAACCTCGTGCCTAACAGTACTACGGCAGGGCAGCAGGCTGCACCTGTGACAGCGGGACTACAAGCTC
 AGCCTGGCGGAGCGCGGAAAAACTCTCAAGAAGAAGTACAAGGCCAGCTATGTCGCTCCATCC
 CTCACTGGGCCATCGAGGTGGACGGCAGGGCTGTACACAGTAGGCTGGGTGATGCCGCCAGCCCC
 CCAAGCGGCCACTGGCAGGGGCCCTGAGGACCAAGATGACAAGGATGGTGGGACTTCAGTGGCACTGGAGGC
 CTTCCGACTACTCAGGCCAACCCATAAAGTGAACACATCGGTGCTACATCCTAGAGAACGACACAGTCCA
 GTGTGACCTGGACCTGTACAAGTCCCTGCAAGGCCCTGAAAAGACACAGTCACATCGACAGGAGATTGAAA
 CCCTGCAAGAACAAAATTAAAGAACCTGAGGGAAAGTCCGAGGTCTGAAAGAAAAGGCCAGAACAGAATGTGAC
 TGTCAAAAATTACGCTTACCAACACCCAGCACAAGGCCCTCAAGCACAGAGGCTCCAGTCTG
 CACATCCTTCA
 GAAGGGCTGCAAGAGAACGGACAGGTGGCTGTGCGGGAGCAGAAGCGCAAGAAGAAACTCCGCAAGCTG
 TCAAGCGCTGCAAGAACACGACACGTGCAAGCATGCCAGGCCCTACGTGCTTCA
 CACAGAACACTGGGACTGCAAGGAGCTGCAAGGGTTACAAGCAGTGTAAACCCCGACTGAAACATGG
 ACCTGGATGGGAGTCTCAACCAGCTACAGTACAGCT
 CTCATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAAACCCCGACTGAAACATGG
 ACCTGGATGGGAGTCTCAACCAGCTACAGTACAGCT
 AAGCTATGAGCAATACAGGCAGTTCAAGCAGTGTGAAAGTGGCAGAAATGAAGAGACCTTCTCCA
 AATCACTGG
 GACAACAGTGGGAAGGCTGGGAAGGT**TAA**AAACACAGAGGTGGACCTCCAAA
 AACATAGAGGCATCACCTGA
 CTGCA
 CAGAGGCAATGAAAAGAACATGTGGGTGATTTCAGCAGACCTGTGCTATTGGCAGGAGGCTGAGAAAGC
 AAGCACGCACTCTCAGTCAACATGACAGATTCTGGAGGATAACCAGCAGGAGCAGAGATAACTCAG
 AAGTCC
 ATTTTTGCCCTGCTTGGATTACCTCAGCAGTCACAAATGCATTTC
 CGTATCAAAAGTC
 ACCACTAACCTCCCCAGAAGCTCACAAGAAAACGGAGAGAGCGAGCAGAGAGATTT
 CCTGAAATTTC
 TCCCAAGGGCGAAAGTCATTGAAATTTC
 AAATCATAGGGAAAAGCAGTCCTGCTATTGGCAGGAGGCTGAGAAAGC
 TTGTTTGTCACAAAGAAGGAAC
 TAAGAACGAGCAGGAGCAGAGGCAACGTGGAGAGGCTGAAA
 ACAGTGCAGAGACG
 TTTGACAATGAGTCAGTACGACAAAAGAGATGACATTAC
 TAGCACTATAACCC
 CTGCTTCA
 TGTGAAAG
 AACCTG
 GCTCTG
 GAGGAGTGGTGTCAATAAACGCTCTG
 GGGCAGTGTAAAAGAAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFTPMCCPSRSSILTGKYVHNHNTYTNNECSPSWQAQHES
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEVGLLKNSRFNYTLCRNGVKEKGSD
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFNASQHITP
SYNYAPNPDKHWIMRYTGPMPKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQGLVKGKSMFYEFDIRVPFYVRGPNEAGCLNPHIVLNIDLAPTI
AGLDIPADMKGKSILKLLDTERPVNRFHKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLKLHKCKGPMRLGGSRALSNLVPKY
YGQGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQ
PRNLTKRHWPGAPEDQDDKDGGDFSGTGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKRPEECDCCHKISYHTQHKGRLKHRGSSL
HPFRKGLQEKDVKWLLREQKRKKKLRKLLKRLQNNNTCSMPGLTCFHDNQHWQTAPFWTLG
PFCACTSANNNTYWCMRTINETHNFLCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPENKRPSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCACTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCCCTGCTGCTGCTGCTGCTGGCCACC
TGCCTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGAAA
CCGAGTCGCCGGGCCAGCCTGGCCCTTCCGGCGCGGGGCCACCTGGGAATCTTCACC
ATCACCGTCATCCTGCCACGTATCTCATGTGCCGAATGTGGCCTCCACCACCAAC
CCCCGCCACACCCCTCACCAACCTCACCACCACCACCCCCACCGCCACCATCCCCGCCA
CGCTCGCTGAGGCTGCTGTCGCCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCATCTG
TTCCCAGGACAAGTGGACCCCATGTTCCATGTGGAAGGATGCATCTCTGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTGCATGGCATGCCCATGTTGGAGAGCAAGG
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTGGGGAGTGGAGAGCAAGG
GTGCTCTTCGGGGCTGGACAGCCCGTCTTGACAGTGACTCCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTT
GGTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTGACCGTGCCTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGAAVAVLLLLLLATCLFHGRQDCDVERNRTAAGGNVRRAQPWPFR
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHLHHHHHPRHHPRHAR

FIGURE 50

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGATCCAGAGCC**ATG**TGGACCTGCTA
CTACTGGGCTGATTGGGGCCTGACTCTTACTGCTGCTGACGCTGCTGCCCTTGCCGG
GTACTCAGGGCTACTGGCTGGGTGGAAGTGAGTGCTGGTCACCCCCCATCCGAACGTCA
CTGTGGCCTACAAGTTCCACATGGGCTCTATGGTGAGACTGGCGGCTTCACTGAGAGC
TGCAGCATCTCTCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
CCCTGATAAGTGCCGATGTGCCGTGGCAGCATTCTGAGTAAGGTGAGGAATGCCCTCCC
CTGAGCTCATCGACCTTACCAAGAAATTGGCTTCAAGGTGTTCTCCTCCGGCACCCAGC
CATGTGGTGACAGCCACCTTCCCTACACCACCAATTCTGCCATCTGGCTGGCTACCCGCCG
TGTCCATCCTGCCCTGGACACCTACATCAAGGAGCGGAAGCTGTGTCCTATCCTCGGCTGG
AGATCTACCAGGAAGACCAAGATCCATTTCATGTGCCACTGGCACGGCAGGGAGACTTCTAT
GTGCCCTGAGATGAAGGAGACAGAGTGGAAATGGCGGGGCTTGTGGAGGCCATTGACACCCA
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTCTGTAAGCTTGGAAAGTGAGCC
CTGGCAGCCGGAGACTTCAGCTGCCACACTGTCACCTGGCGAGCAGCCGTGGCTGGAT
GACGGTGACACCGCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGCTCCTTTGA
GGAGCTGGACTTGGAGGGCGAGGGCCCTAGGGAGTCACGGCTGGACCTGGACTGAGC
CCCTGGGACTACCAAGTGGCTTGGAGGCCACTGCCCTGAGAAGGGCAAGGGAG**TAA**CC
ATGGCCTGCACCCCTCTGCAGTGCAGTTGCTGAGGAACGTGAGCAGACTCTCCAGCAGACTCT
CCAGCCCTTCCCTCCTCTGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCTG
TCCAGGCCTTGTCTAACGCTTCTCCTACTGCCCTTAGGCTCCAGGGCAGAGGAGCCA
GGGACTATTTCTGCACCAGCCCCAGGGCTGCCCTGTTGTCTTTTCAAGACTC
ACAGTGGAGCTCCAGGACCCAGAATAAGCCAATGATTACTGTTCACCTGGAAAAAAA
AAAAAAAAAAA

FIGURE 51

MSDLLLGLIGGLTLLLLLTLAFAAGYSGLLAGVEVSAGSPPIRNVTVAYKFMGLYGETGR
LFTECSISPKLRSIAVYYDNPHMVPDKRCAVGSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTIILSIWLATRRVHPALDTYIKERKLCAYPRLIEIQEDQIHFMCPALAR
QGDFYVPEMKETEWKWRGLVEAITQVDGTGADTMSDTSSVSLLEVSPGSRETSAAATLSPGAS
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGPLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

FIGURE 52

CCGCAGGAACGCTGTCTGGCTGCCGCCACCGAACAGCCTGTCTGGTCCCCGGCTCCCT
GCCCGCGCCCAGTCATGACCCCTGCGCCCTCACTCCTCCGCTCCATCTGCTGCTGCT
GCTGCTCAGTGCGCGGTGTGCCGGCTGAGGCTGGCTCGAAACCGAAAGTCCGTCCGGA
CCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCGCTGCTTTGGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCTCTGGTTATAGAACTTGGCAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGGAGAGAACGCAAGGGCAATCATTCTCACTTGGCCTAT
GGAAAACGGGGATTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACTAATCCGAGCCAACTAAGCTGGCTAAAGCTGGTGAAGGGCATTTGCCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCTGGCCTCATTGGGTATCACCTATAAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAACGAAACAAGAGCAAAAGAAATA
ATAAATAATAAATTTAAAAAACTTAAAAAAAAAAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLSSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVI PGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKGILPLVGMAVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

FIGURE 54

CCCGGGAACGTGTTCTGGCTGCCGCACCGAACAGCCTGTCCTGGTGCCTGGCTCCCTGC
CCCGCGCCCAGTCATGACCTGCGCCCCCTCACTCCTCCGCTCCATCTGCTGCTGCTGC
TGCTCAGTGCAGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCCTGGACC
CTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCGCTGCTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGAGACCCCTGGTTATAGAACCTGGCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGGAGAGAACGGAAGGGCAATCATTCTCACTTGGCCTATGG
AAAACGGGGATTCACCCTGTCCCAGCGGATGCAGTGGTCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACACTGGCTAAAGCTGGTAAGGGCATTTCCTCTGGTAGGG
ATGGCCATGGTGCCACCCCTCCTGGCCTCATTGGTATCACCTATAAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAAGAGCAAAAGAAATAATA
AATAATAAATTTAAAAACTTA

FIGURE 55

CCGAAAGTCCC GTCCGGAC CCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCCTCTGGTATAGAACTTGGCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTCTCGACATGTGTGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTCCACCATCTGTCCCAGCGGATGCAGTG
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCA ACTACTGGCTAAAGCTGGTGAAGG
GCATTTGCCTCTGGTAGGGATGCCATGGTGC CAGCCCTCCTGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAACGAAA
CAAGAGCAAAAGAAATAATAATAATAAATTTAAAAAAACTTAAAAA

FIGURE 56

CTGCTGCATCCGGGTGTCGGAGGCTGTGCCGTTTCTGGCTAAATCGGGGAG
 TGAGGCAGGCCGGCGCGACACCGGGCTCCGGAACCACGTGACGACGGGCTGGACTG
 ACCTGAAAAAA**ATG**TCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGG
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTATCCCACCATGAAAGATTCACCACCTACACCATGCCT
 GTGGTGTATAGCAACCATAGCCTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGTCTGGTCAAACAGGTGCTCGCATTGGCTTTCGTTGG
 TTTCATGTTGCCCTTGGATCTCTGATTGCATCTATGTGGATTCTTTGGAGGTTATGTTG
 CTAAAGAAAAAGACATAGTATAACCTGGAATTGCTGTATTTTCCAGAATGCCTCATCTT
 TTTGGAGGGCTGGTTTAAGTTGCCGCACTGAAGACTTATGGCAG**TGA**ACACATCTGAT
 TTCCCACAGCACAAACAGCCCTGCATGGTTGTTTTACTGCTCACTCCAACCTT
 TTGTAATGCCATTCTAAACTTATTCTGAGTGTAGTCTCAGCTAAAGTTGTGAATAACT
 AAAATCAGGAGAACACCTAAACAACCAAAAAATCTATTGTGGTATGCACTTGATTAACCT
 ATAAAATGTTAGAGGAAACTTCACATGAATAATTTGTCAAATTTATCATGGTATAATT
 TGTAAAAATAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTGTCATA
 TCTGAGGTCCAAACCACAATGAAAGTGCTCTGAAGATTAAATGTGTTATTCAAATGTGGT
 CTCTCTGTGTCATGTTAAATGAAATATAACATTAGTTAAATGTTAAAATATTCCGTGG
 TCAAAATTCTCCTCACTATAATTGGTATTACTTTACCAAAAATTCTGTGAACATGTAAT
 GTAACTGGCTTGAGGGTCTCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAACCAT
 GGTCCAGGCCACCAGGCTCCCTGTGTCCTCCATGGGAAGGTCTCCGCTGTGCCTCTCATT
 CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTCTGGTGGATGCACAGTCACTC
 CACATCCACCACTG

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIIDAAVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFGMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFGGGLVFKFGRTEDLWQ

FIGURE 58

TTCTGGCTAAAATCGGGGGAGTGAGGCAGGCCGCGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTATCCCACCATGAAAGAT
TTCAACCACCTACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCAATGATTAATGC
AGTATCGAACATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTGGCTTTCGTTGGTTCATGTTGGCCTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATAACCCTGGAATTGCTGTATT
TTTCCAGAATGCCTTCATCTTTGGAGGGCTGGTTTAAGTTGGC

FIGURE 59

TGGACGGACCTGAAAAAAATGTTGGATTNTAGAGGGNTGAGATGTCAGAATGCATGAC
TGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTATCCCACCATGAAAGATTCAACCANTCATACC
ATGCCTGTGGTGTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGGTGGTCAAACAGGTGCTCGCATTGGCTTT
CGTTGGTTCATGTTGGCCTTGGATCTCTGATTGCATCTATGTGGATTCTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCCTGGAATTGNTGTATTCCAGAATGCCTTC
ATCTTTTGAGGGCTGGTTAAGTTGGCCGCAGTGAAGANTATGGCAGTG

FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGTGGANTGACCTGAAAAAAATGTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATA
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTGGCTTCGTTGGTTCATGTTGGCCTTGGATT
CTGATTGNATTCTATGCGGATTCTTCTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTCCAGAATGCC

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTNAACCANTCATACCATGCCTGTGGTGTATAGCAACCATAAGCC
TTCCTAACATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTGGCTTNGTGGTTCATGTTGGCCTTGGATCTN
TGATTGCATTATGTGGATTNTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

FIGURE 62

GGGAGGGCTGTGNCCGTTTGGCTAAATCGGGGGAGTGAGGCGCCGGCGCG
CGNGACACCAGGGTCCGGGAACCATTGCACGACGGGGTGGACTGACCTGAAAAAAATGTTG
GATTNTAGAGGGCTTGAGATGCTCAGAACATGCATTGACTGGGGAAAAGCGCAATACTATT
GCTTCATTGCTGCTGGTGTACTATTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTCAACCACCTACATACCATGCCTGTTAGCAACCA
TAGCCTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGTCTGGGTCAAACAGGTGCTCGCATTGGCTTCTGTTGTTCATGTTGGCCTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCCTGGAATTGCTGTATTTCCAGAACATGCCTTCATNTTTGGAGGCTG

FIGURE 63

CGACGCCGGCGT**TAG**TGGCTTCCGCTGGTGTGCTCCTGGCTGTGCTGCTGGCCGTCC
 TCTGCAAAGTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTCTCCGAAGATGTC
 AAACGGCCCCCAGCGCCCCCTGGTAACTGACAAGGAGGCCAGGAAGAAGGTTCTCAAACAAGC
 TTTTCAGCCAACCAAGTGCCGGAGAAGCTGGATGTGGTGGTAATTGGCAGTGCGTTGGGG
 GCCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCCTGGTGTGGAACACAAT
 ACCAAGGCAGGGGGCTGCTGTACACCTTGGAAAGAATGGCCTTGAATTGACACAGGAAT
 CCATTACATTGGCGTATGGAAGAGGGCAGCATTGGCGTTTATCTGGACCAGATCAGTG
 AAGGGCAGCTGGACTGGGCTCCCTGTCCCTCTTGCACATCATGGTACTGGAAGGGCCC
 ATGGCCGAAAGGAGTACCCCCATGAGTGGAGAGAAAGCCTACATTAGGGCCTCAAGGA
 GAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATAAAGCTGGTTAAGGGTGTATCA
 GTGGAGCCCCCTCATGCCATCCTGTTGAAATTCTCCATTGCCGTGGTCAAGCTCCTCGAC
 AGGTGTGGGCTGCTGACTCGTTCTCCATTCTCAAGCATCCACCCAGAGCCTGGCTGA
 GGTCTGAGCAGCTGGGGCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTCCCCA
 CTTACGGTGTACCCCCAACACAGTGCCTTCCATGCACGCCCTGCTGGTCAACCAACTAC
 ATGAAAGGAGGCTTTATCCCGAGGGGGTCCAGTGAAATTGCCCTCACACCACCTGT
 GATTCAAGCGGGCTGGGGCGCTGTCCACAAAGGCCACTGTGCAAGAGTGTGTGCTGGACT
 CAGCTGGGAAAGCCTGTGGTGTAGTGTGAAGAAGGGCATGAGCTGGTGAACATCTATTGC
 CCCATCGGGTCTCAACGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGAACGC
 CCGCTGCCAGGTGTGAAGCAGCAACTGGGACGGTGCAGGCCGGCTTAGGCATGACCT
 CTGTTTCTCATCTGCCATGCCAGGCAACAGGAAGACCTGCATCTGCCGTCCACCAACTACTAT
 GTTACTATGACACGGACATGGACCGAGGCGATGGAGCGTACGTCTCCATGCCAGGGAAAGA
 GGCTCGGAACACATCCCTCTTCTCTTCCATCAGGCAAAGATCCGACCTGG
 AGGACCGATTCCCAGGCCGGTCCACCATGATCATGCTCATACCCACTGCCCTACGAGTGGTT
 GAGGAGTGGCAGGCCGGAGCTGAAGGGAAAGCAGGGCAGTGACTATGAGACCTTAAAAACTC
 CTTGTGGAAGCCTCTATGTCAGTGGCCTGAAACTGTTCCACAGCTGGAGGGAAAGTGG
 AGAGTGTGACTGCAGGATCCCCACTCACCAACCAAGTTCTATCTGGCTGCTCCCCGAGGTGCC
 TGCTACGGGGCTGACCATGACCTGGGCCCTGCACCCCTGTGTGATGCCCTCTGAGGGC
 CCAGAGCCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTCACCTGTGGACTGGTCG
 GGGCCCTGCAAGGTGCCCTGCTGTGCAGCAGGCCATCCTGAAGCGGAACTGTACTCAGAC
 CTTAAGAATCTGATTCTAGGATCCGGCACAGAAGAAAAAGAAT**TAG**TTCCATCAGGGAGG
 AGTCAGAGGAATTGCCAATGGCTGGGCATCTCCCTGACTTACCCATAATGTCTTCTG
 CATTAGTTCTTGACGTATAAAGCACTCTAATTGGTCTGATGCCCTGAAGAGAGGCC
 TTAAATCACAATTCCGAATCTGGGCAATGGAATCTGCTCCAGTGGGCAAGGTGAGA
 TCTTACGCCTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGATG
 TCTCATGACGAGCGCGCTGCACTCCCTACCCATGCCCTAACACTCAGTGATCAAAGCGA
 ATATTCCATCTGGGATAGAACCCCTGGCAGTGTGTCAGCTAACCTGGTGGGTTCAAGTTC
 TGTCTGAGGCTCTGCTCTCATTCTAGTGCTACGCTGCACAGTTCTACACTGTCAAGG
 GAAAAGGGAGACTAATGAGGCTTAACCTAAACCTGGGCGTGGTTGGTGCATCCATA
 GTTTGGAGAGCTAGATCTCTTGCTGGGTTCACTGGCTCTTCAGGGGACAGGAAAT
 GCCTGTGCTGGCCAGTGTGGTTCTGGAGCTTGGGTAACAGCAGGATCCATCAGTTAGTA
 GGGTGCATGTCAGATGATCATATCCAATTGATGAGGCTTAACCTGGGCGTGGTTGGTGC
 TCAGGGTGGCAGCTGGTTCTCAATGTCAGGCCAGGGACTCAGTACCTGAGCCTCAATCAAGC
 CTTATCCACAAATACACAGGGAAAGGGTGTGAGCAGGGGACATCAGGAGTCAGGGCA
 TGGACTGGAAGATGAATACTTGCTGGGCTGAAGCAGGCCAGGGCATTCCAGGCAAGGG
 CACAGCAGGGGACAGTGCAGGGAGGGTGTGGGTAAGGGAGGGAAAGTCACATCAGAAAAGGG
 AAGCCACGGAATGTGTGAAGGCCAGAAATGGCATTGCAAGGTTGGAAAAATGACTTT
 TAGACAGGTAGGTGAATGCAAGCTCAAGGTTGGAAAAATGACTTTCAAGTTATGTGAGGG
 GTATCAGACATACGAAAGGTCTTTGTAGTTGTTAATGTAACATTAATAAATTATTG
 ATTCCATTGCTTAAAAAAAAAAAAAA

FIGURE 64

MWLPLVILLAVLLAVLCKVYLGLFSGSSPNPFSEDVKRPPAPLVTDKEARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPISSPFDIMVLEGPNRKEYPMYSGEKAYIQGLKEKFPO
EEAIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
GGAVLTKATVQSVLDSAGKACGVSVKGHELVNIYCPIVVSAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGKEDLHLPSTNYVYYDTMDQAMERYVSMPREEAAEH
IPLLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEWQAEKGKRGSDYETFKNSFVEA
SMSVVLKLFQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKNN

FIGURE 65

GCAGCGGCGAGGC GGCGGTGGCTGAGTCGTGGCAGAGGCGAAGGCGACAGCTCTA
 GGGGTTGGCACCGGCCCGAGAGGAGGAGT**G**CGGGTCCGGATAGGGCTGACGCTGCTGTG
 TCGGGTGTGCTGAGCTTGGCCTCGCGTCCTCGGATGAAGAAGGCAGCCAGGATGAATCCT
 TAGATTCCAAGACTACTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA
 GTAGTTGCTGGTCAAATATTCTTGTGATTCAAGAAGAATCTGAATTAGAATCCTCTATTCAAGA
 AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAGAAGATATCAGCTTCTAG
 AGTCTCCAATCCAGAAAACAAGGACTATGAAGAGCCAAGAAAGTACGGAAACCAGCTTG
 ACCGCCATTGAAGGCACAGCACATGGGAGCCCTGCCACTTCCCTTTCTTAGATAA
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTGCTACAACCT
 ATGACTACAAAGCAGATGAAAAGTGGGCTTTGTGAAACTGAAGAAGAGGCTGCTAACAGA
 CGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGAATGAAATCCTTAATGGAAGCAA
 TAAGAAAAGCCAAAAAAGAGAAGAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA
 CCAAAGCCCTGGAGAGAGTGTCAATGCTCTTATTGGTGATTACTGCCACAGAATATC
 CAGGCAGCGAGAGAGATGTTGAGAAGCTGACTGAGGAAGGCTCTCCAAGGGACAGACTGC
 TCTTGGCTTCTGTATGCCCTGGACTTGGTGTATTCAAGTCAGGCAAAGGCTTGTAT
 ATTATACATTGGAGCTCTGGGGCAATCTAACAGCCCACATGGTTGGTAAGTAGACTT
TAGTGGAAGGCTAATAATTTAACATCAGAAGAATTGTGGTTATAGCGGCCACAACCTT
 TCAGCTTCATGATCCAGATTGCTTGTATTAAGACCAAATTCAAGTGAACCTCCTCAA
 ATTCTTGTAAATGGATATAACACATGGAATCTACATGTAATGAAAGTTGGTGGAGTCCACA
 ATTTTTCTTAAATGATTAGTTGGCTGATTGCCCTAAAAGAGAGATCTGATAAATGGC
 TCTTTTAAATTTCTGTAGTTGGAATTGTCAGAACATTTTACATTAGATTATCATAA
 TTTAAAAATTCTTGTAAATGGCTATAGAAAACAACAT
 GAAATATTACAAATTTGCAACAATGCCCTAAGAATTGTTAAATTCATGGAGTTATT
 GTGCAGAACATGACTCCAGAGAGCTCTACTTCTGTTTACTTTCATGATTGGCTGTCTC
 CCATTTATTCTGGTCATTATTGCTAGTGACACTGTGCCTGCTCCAGTAGTCTCATTTC
 CTATTTGCTAATTGTTACTTTCTTGCTAATTGGAAGATTAACTCATTAAATAAA
 ATTATGTCTAAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAA

FIGURE 66

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLDSTTLTSDESVKDHTTAGRVVAGQIFLD
SEESELESSIQEEEDSLKSQEGERVTEDISFLESPNPNKDYEEPKKVRKPALTAIEGTAHG
EPCHFPFLFLDKEYDECTS DGRDGRLWCATTYDYKADEKWGFCETEEAAKRRQM QEAEMM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLQPNIQAAREMFEK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLIAHMVLVSRL

FIGURE 67

CTTCCCAGCCCTGTGCCCAAAGCACCTGGAGCATATAGCCTGCAGAACTTCTACTTGCGCT
GCCTCCCTGCCTCTGGCC**ATG**GCCTGCCGGTGCCTCAGCTCCTCTGATGGGACCTCCT
GTCAGTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTACCACAGGGACTACGGTGTGCCTGG
TACCAGCAGCAGGGCAGGCAGTGCCCTCGATATCTCCTCTACTACCGCTCGGAGGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGGATGAGGCCACAATGCCT
GTGTCCTCACCATTAGTCCCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTAGTCCC**TAG**GGGTGGGTGTGAGATGGGTGCCTCCCTCGCCTCCCATTCT
GCCCTGACCTTGGGTCCCTTTAACTTCTCTGAGCCTGCTCCCTCTGTAAAATGGG
TTAATAATATTCAACATGTCAACAAAC

FIGURE 68

MACRCLSFLLMGTLSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP

FIGURE 69

GCCGCCCCGCCCGAGACCGGGCCGGGGCGCGGGCGGGATGCGGCGCCGGGGCG
 CGATGACC CGGGAGCGCACGCCGCGGGCCCGCTGACCCCGCCGCCGCTGAGGCC
 CCCGCCGAGGTCCGGACAGGCCGAG**ATG**ACGCCGAGCCCCCTGTTGCTCTGCTGCCGC
 CGCTGCTGCTGGGGCCTTCCCACCCGCCGCCGCCGAGGCCAAAGATGGCGGAC
 AAGGTGGTCCCACGGCAGGTGGCCCGCTGGCCGCACTGTGCGGCTGCAGTGCCCAGTGG
 GGGGGACCCGCCCGCTGACCATGTGGACCAAGGATGGCCGCACCATCCACAGCCGCTGGA
 GCCGCTTCCCGCTGCTGCCGCAGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCCGC
 GTGTACGTGCAAGGCCACCAACGGCTTCGGCAGCCTGAGCGTCAACTACACCCCTCGTGT
 GCTGGATGACATTAGCCCAGGGAGAGGACTGGCCAGCAGCTCTGGGGTCAAG
 AGGACCCGCCAGCCAGTGGGACGACGCCCTGGGCCCCAGAGGATGAGGCGC
 CGGGTGATCGCACGGCCCGTGGTAGCTCCGTGCCGCTCAAGTGCCTGCCAGCGGGCACCC
 TCGGCCCGACATCACGTGGATGAAGGACGACCAGGCCCTGACGCCAGAGGCCGCTGAGC
 CCAGGAAGAAGAAGTGGACACTGAGCCTGAAGAACCTGCGGCCGGAGGACAGCGGCAAATAC
 ACCTGCCCGTGTGCAACCGCGCGCCATCAACGCCACCTACAAGGTGGATGTGATCCA
 GCGGACCCGTTCCAAGGCCGTGCTCACAGGCACGCACCCGTGAACACAGACGGTGGACTTCG
 GGGGGACCACGTCCCTCCAGTGCAAGGTGCGCAGCAGCTGAAGCCGGTATCCAGTGGCTG
 AAGCGCGTGGAGTACGGCGCCGAGGGCCGACAACACTCCACCATCGATGTGGGGCCAGAA
 GTTGTTGTGGTGTGCCCACGGGTGACGTGTGGTCGCGGCCGACGGCTCTACCTCAATAAGC
 TGCTCATCACCGTGCCGCCAGGACGATGCCGGCATGTACATCTGCCCTGGGCCAACACC
 ATGGGCTACAGCTCCCGCAGGCCCTCCACCGTGTGCCAGACCCAAAACGCCAGGGCC
 ACCTGTGGCCTCTCGGCCACTAGCCTGCCGTGGCGTGGTATCGGCATCCCAG
 CCGGCCGCTGTCTTCATCCTGGGACCCCTGCTCCTGTGGCTTGCAGGGCAGAAGAACCG
 TGCACCCCGCGCCTGCCCTCCCTGCCCTGGCACCGCCGCCGGGACGGCCGACCG
 CAGCGGAGACAAGGACCTCCCTCGTTGGCCGCCCTAGCGCTGGCCCTGGTGTGGGCTGT
 GTGAGGAGCATGGGTCTCCGGCAGCCCCCAGCACTACTGGGCCAGGCCAGTTGCTGG
 CCTAAGTTGACCCAAACTCTACACAGACATCCACACACACACACACACTCTCACAC
 ACACTCACACGTGGAGGGCAAGGTCCACCAGCACATCCACTATCAGTGT**TAG**ACGGCACCGT
 ATCTGCAGTGGGACGGGGGGCCGGCCAGACAGGCAACTGGGAGGATGGAGGACGGAGCT
 GCAGACGAAGGCAGGGACCCATGGCAGGGAGGAATGCCAGCACCCAGGCAGTGTGTG
 TGAGGCATAGCCCTGGACACACACAGACACACTACCTGGATGCATGTATGCAC
 ACACATGCGGCACACGTGCTCCCTGAAGGCACACGTACGCACACGCACATGCACAGATATG
 CCGCCTGGGACACAGATAAGGCCAAATGCACGCACACCGTGCAGATGTGCTGCCGGACA
 TACAAGGACATGCTGCCCTGAACATACACACGCACACCGTGCAGATATGGTATCCGGACACA
 CACACACACACAGGATATGCTGCTGGACACACAGATAATGCTGCCCTGACACACACATGCACGG
 ATATTGCCCTGGACACACACACACACAGCTGCAGATATGCTGCTGGACACAC
 ACATGCAGATATGCTGCCCTGGACACACACTTCCAGACACACGTGCACAGGCCAGATATGCT
 GCCTGGACACACGCAGATATGCTGCTAGTCACACACACGCAGACATGCTGCCGGACAC
 ACACACGCATGCACAGATATGCTGTCGGACACACACACGCACGCAGATATGCTGCCGGAC
 ACACACACAGATAATGCTGCCCTAACACTCACACAGCTGCAGATATTGCCCTGGACACACACA
 TGTGCACAGATATGCTGCTGGACATGCACACACAGCTGCAGATATGCTGCCGGACACAC
 CACGCACACATGCGAGATATGCTGCCCTGGACACACACTCCGGACACACATGCACACACAGT
 GCAGATATGCTGCCCTGGACACACACAGATAATGCTGCCCTAACACTCACACACGTGCAGA
 TATTGCCCTGGACACACACATGTCAGATATGCTGCTGGACATGCACACACAGCTGCAGATA
 TGCTGCCGGATACACACGCACACATGCAGATATGCTGCCCTGGACACACACTTCCGG
 CACACATGCACACACAGGTGCAGATATGCTGCCCTGGACACACGCAGACTGACGTGCTTTGG
 GAGGGTGTGGCTGAAGCCTGCAAGTACGTGTGCCGTGAGGCTCATAGTTGATGAGGGACTTT
 CCCTGCTCCACCGTCACTCCCCAACTCTGCCGCCCTGTCCCCGCCCTAGTCCCCGCC
 CATCCCCGCCCTGTCCCCCTGGCCTGGCGCTATTGGCCACCTGCCCTGGGTGCCAGG
 AGTCCCCACTGCTGTGGCTGGGTTGGGGCACAGCAGCCCCAAGCCTGAGAGGGCTGGAG
 CCCATGGCTAGTGGCTCATCCCCAGTGCATTCTCCCCCTGACACAGAGAAGGGCTTGGTA
 TTTATATTAAGAAATGAAGATAATTTAATAATGATGGAAGGAAGACTGGGTTGCAGGGAC
 TGTGGTCTCCTGGGGCCGGGACCCGCCCTGGTCTTCAGCCATGCTGATGACACACAC
 GTCCAGGCCAGACACCACCCCCCACTGCTGTGGTGGCCCCAGATCTGTAAATT
 TGTAGAGTTGAGCTGAAGCCCCGTATATTAAACACACAAAA

FIGURE 70

MTPSPLLLLLPPLLGAFFPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTIHSGWSRFRVLHQGLKVQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDISPGK
ESLGPDSSSGQEDPASQQWARPRFTQPSKMRRVIARPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSSA
TSLPWVIVIGIPAGAVFILGTLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGSPAAPQHLLGPgpVAGPKLYPKLYTDIHTHTHSHTHVEGKV
HQHIHYQC

FIGURE 71

CCCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAAACTTCCCAGGGGACCGCATTCCAGAGTC
 AGTGACTCTGTGAAGCACCCACATCTACCTTGCACGTTCCCACGGGCTTGGGGAAAG**ATGGTGGGACCA**
 AGGCCTGGGTGTTCTCCTCTGGTAAGTCACATCTGTGTTGGGAGACAGACATGCTCACCCAGTC
 GTAAGAAGAGTCCAGCCTGGGAAGAAGAACCCAGCATCTTGCACAGGCTGCCACCCCTGGAGAGGCCCTGG
 TGACTGGACAACATGGTCAACATCGACTACCCAGGGAGGGCGACTATGAGCGGCTGGACGCCATTGCT
 TCTACTATGGGACCGTGTATGTGCCGCCCCCTGCGGCTAGAGGCTCGGACCACTGACTGGACACCTGCCGGC
 AGCACTGGCCAGGTGGTCCATGGTAGTCCCCGTGAGGGTTCTGGTGCCTCAACAGGGAGCAGGCCCTGGCCA
 GAACTGCTCTAATTACACCCTACGCTTCCCTGCCAACAGGATCCTGCCGGAGACACAGAGCGCATCTGGA
 GCCCATGGTCTCCCTGGAGCAAGTGTCACTGCCGTGGTAGACTGGGGTCCAGACTCGCACACGCATTGCT
 TTGGCAGAGATGGTGTGCGTGTGCACTGAGGCCAGCGAAGAGGGTCAAGACTGCATGGGCCAGGACTGTACAGC
 CTGTGACCTGACCTGCCAATGGGCCAGGTGAATGCTGACTGTGATGCCATGTGCCAGGACTTCATGCTTC
 ATGGGGCTGTCTCCCTCCGGAGGTGCCCGCCTCAGGGGCTGTCTACCTCTGGACCAAGAGGCCGAAG
 CTGCTGACCCAGACAGACAGTGTAGGGAGATTCCGATCTCCCTGGCTTGTGCCCTGATGGCAAAGCATCTGAA
 GATCACAAAGGTCAAGTTGCCCCATTGTACTCACAATGCCCAAGACTAGCCTGAAGGAGGCCACCATCAAGG
 CAGAGTTGTGAGGGCAGAGACTCCATACATGGTAGTAACCCAGACAAAAGCACGGAGAGCTGGGAGAGC
 GTGTCTCTGTGCTTAAGGCCACAGGGAGGCCAGGACAAGTATTGGTATCATAATGACACATTGCT
 GGATCCTCCCTCTACAAGCATGAGCAAGCTGGTGTGAGGAAACTGCGCAGCACCCAGGCTGGGAGTACT
 TTTGCAAGGCCAGAGTGTGCTGGGCTGTGAAGTCAAGGTGCCCAGCTGATTGTACAGCATCTGAG
 ACTCCTTGCACCCAGTCTCTGAGAGCTATCTTATCCGCTGCCCATGATTGCTTTCAGAATGCCACCAACTC
 CCTTACTATGACGGGAGCCTGCCCTGAGACTGGCAGGGCAGCAGGATAATGGGATCAGGTGCCGTG
 ATGCTGTGCAAGACTGCTGGCATCTCCAAAGACAGGGAGGAGTCCACTGCACTGGCTACAGCTACCGCTACCC
 ACCAAGGGGCCAAGGAGTGCAGCTGCCAGGGTGTACGGAAACTCGGAGCATCGTGGGGGCCGTGAGTGC
 TGCTGACAATGGGAGGCCATGCGTTTGCCATGTGACATGGGAACAGCCGTGTAAGCATGACTGGCTACA
 AGGGCACTTCACCCCTCATGCCCCCAGACACTGAGGGCTGTGTCACATTGTTGGACAGGCTGAGAAG
 TTTGTCACACCACCAAAAGTGTCACTTCAACAGAAGGGGAGTGGCGTGTCCATGAAATCAAGATGCTTCG
 TCGGAAAGAGCCCATCATTGAGGCCATGGAGACCAACATCATCCCCCTGGGGAAAGTGGTGGTGAAGACC
 CCATGGCTGAACTGGAGATTCCATCCAGGAGTTCTACAGGCAGAATGGGAGCCCTACATAGGAAAGTGAAG
 GCCAGTGTGACCTTCTGGATCCGGAAATTTCCACAGGCCACAGCTGCCAGACTGACCTGAACTTCATCAA
 TGACGAAAGGAGACACTTCCCCCTCGCACGCTATGGCATGTTCTGTGACCTTGAGGATGAGGTGACCTCAG
 AGCCACTTAATGCTGCAAAGTGAAGGTCCACCTGACTCGACCCAGGTCAAGATGCCAGAGCACATATCCACA
 GTGAAACTCTGGTCACTCAATCCAGACACAGGGCTGTGGGAGGGAGGAAGGTGATTCAAATTGAAAATCAAAG
 GAGGAACAAAAGAGAAGACAGAACCTCCGGAACTCTGGGGCAACCTGGAGATTGAGAGGAGGCTCTTAACCTGG
 ATGTTCTGAAAGCAGGGCGTGTGTTGTAAGGTGAGGGCTACGGAGTGGAGGTTCTGGCTAGTGAGCAG
 ATCCAGGGGTTGTGATCTCGTGATTAACCTGGAGCCCTAGAAACTGGCTCTGTGATGACCTGACCTGCTGGG
 CCGCTTGCACAGTGTCACTCACAGGCCAACAGGGGCTGTGTGCGCTGCCCTGTGATGACCTGACCTGATG
 CCTACTCTGCCTATGCTTGGCAAGGCTGCTGGGGAGGAACGTCAAGCAGTGGAGCTTCTCTCAAATTCAAC
 CCAAATGCAATTGGCGTCCCCCATGCCCTATCTCAACAAAGCTCAACTACCGTGGAGGACCATGAGGATCCACG
 GTTAAAAAGACAGCTTCCAGATTGACATGGCAAGGCCAAAGGCCACTCAGCTGAGGCCACTTCCGGTTCTACCAGATT
 GAGGGGGATGCGATGACTACACACAGTCCCCCTCAACAGAAGATGCCCTATGAGCTGGACTGAAGACTATCT
 GGCATGGGGCCAAAGCGATGGAATTCAAGGGGCTGTGATGAGGTTGAGGAGGCTGGGAGTGGAGTGA
 ATGTCGATCCGCAACATGGGGGCACTCATGGCGGACAGTGGGGAGCTGATGGAGGAGGAGGAGGATGAG
 AGCACTGGGACAGGGACCAGCCAATGTCAGCTGCCGTGCTGGAGTTCAAGTGCAGTGGGATGCTATGA
 TCAGGACCGTGTGGACGCCACCTGGTGAAGGTGATCCCCCAGGGCAGCTGCCGTGAGGCCAGTGTGAAACCCCA
 TGCTGCGATGAGTACCTGGTCAACACTTGCACCTGCACTGCAACACAGCACAGGACTGAGTACACCATGCTGGCA
 CCCTGGACCCACTGGCCACAACATGGCATCTACACTGTCACTGACCCAGGACCTGCCACGCCAAGGAGAT
 CGCGCTGCCGGTGTGTTGATGGCACATCCGATGGCTCCTCCAGAATCATGAAGAGCAATGTGGAGTAGGCC
 TCACCTCAACTGTGAGAGGAGCAAGTAGGCCAGAGTGCCTCCAGTACCTCCAAAGCACCCAGGCCAG
 TCCCTGCTGCCAGGACTGTCACAGGAGGAGTGGCTCTGAGATTCTGCTCAACAGGCCCTGATCAAC**TAA**TTGTG
 ACTTCACCCCTCTGCCCCATTGATGTGACAGCATTGTGAGACTGATGACCAAACACTGTCACCTGGTTAAT
 TTAAGCACCTCTGTTGCTGATGTTGTTCTTCTCATGCTTACTTACTTGTCCCCTGCTACTG
 TTGGCAGCTGGCCCCCACAATGGCACAATAAGCCCCCTTGTGAAACTGTTCTTAAATGAAACACAAGAAAATT
 GCCCACTGGTAAACACTGCACTGACTTCACTGATTTAATGCCATTAAATGCAAATATACTTCCCTTCTT
 TTGCTGATGTTTGCCACCTCTGCAATAGTGATAATCTGATGCTGAGATCAAATAACCAATAAAAGCATAT
 TTCTGGCTTGCTCCACAGGACATAGGCAAGCCTGATCATAGTTCAACATATAAATGGTGGTGAATAAAG
 AAATAAAACACAATAACTTTACTTGAATAACTTAAATAACTTATTATTTCTTGTCAAATTTGGAAATTCTAGTGC
 ACATTCAAAGTATTAAATATAGGGTGTGATCATAGTTCTCATACCAAGTCTGGAAAGAACATCTCCTG
 ATCCACAATTACACCAGGTGCTAAGTGTATTTGACATTCCCTTGCATTGCTTTGTTCTGCTAGAAC
 CAAGTGTAGCCCAGGGCAGATGCAATAATGCATACTCTGTATTCGAAAAAA

FIGURE 72

MVGTKAWVFSFLVLEVTSQLGRQTMLTQS VRRVQPGKKNPSIFAKP ADTLESPGEWTTWFNI
DYPGGKGDYERLDAIRFY YGDRVCARPLRLEARTTDWTPAGSTGQVVHGSREGFWCLNREQ
RPGQNCNSNYTVRFCLCPPGLRRTTERIWSPWSPWSKCSAACGQTGVQTRTRICLAEMVSCLS
EASEEGQHCMGQDCTACDLTCPMGQVNADCACMCQDFMLHGA VSLPGGAPASGAAIYLLTK
TPKLLTQTDSDGRFRIPGLCPDGKSILKITKVKF APIVLTMPKTSLKAATIKA EFVRAETPY
MVMNPETKARRAGQS VSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHE SKLVLRKIQQHQAG
EYFCKAQSDAGAVKS KVAQLIVTASDET PCNPVPESYLI RLPHD C FQNATNSFYYDVGRCPV
KTCAGQQDNGIRCRDAVQNCCGISKTEEREIQC SGYTLPTKVAKECSCQRCTETRSIVRG RV
SAADNGEPMRFGHV YMGN S RVSMTGYKGTFTLHV P QDTERLV LTFVDRLQKFVNTTKVLP FN
KKGS AVFHEIKMLRRKEPI TLEAMETNIIPLGEVVGEDPM AELEIPSRSF YRQNGE PYIG KV
KASVTFLDPRNISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEV TSEPLNAGKV KVHL
DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
DVPESRRCFVKVRAYR SERFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFD SVITGPNGA
CVPAFCDDQSPDAYSAYVI LASLAGEELQAVESSPKFNPNAIGVPQPYLNKL NYRRTDHEDPR
VKKTAFQISMAKPRPNSAEE NGPIYAFENLRACEEAPP SAAHFRFYQIEGDRYDYNTVPFN
EDDPMSWTEDYLAWWPKPMEFRACYIKVKIVGPLEVNVR SRNMGGTH RRTVGKLYGIRDVRS
TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVPI PQGSCRRASVN PMLHEYLVNHLPLAV
NN DTSEYTM LAPLDPLGHNYGIYT VTDQDP RTAKEIALGRCFD GTSDGSSRIMKS NVGVALT
FNCVERQVGRQSAFQYLQSTPAQSPAAGTVQGRVPSRRQQRASRG GQRQGGVVASLRFPRVA
QQPLIN

FIGURE 73

CTGCAAGTGTAAACGCCAACACACAAGTATGTTAGGCTTCACCAAAGCCTCAATATACTGAATACGCAC
 AATATCTTAACCTTCATATTGGTTGGGATCTGTTGAGGTCCCATCTCATTAAAAAAATACAGAG
 ACCTACCTACCGTACGCATACATACATATGTATATATGTAAACTAGACAAAGATCGCAGATCATAAAGC
 AAGCTCTGCTTAGTTCCAAGAAGATTACAAGAATTAGAGATGTATTGTCAAGATCCCTGTCGATTGATG
 CCCTTGGTTACGGTGTCTCAGTGATGCAGCCCTACCCCTGGTTGGGACATTATGATTGTGTAAGACT
 CAGATTTACACGGAAGAAGGGAAAGTTGGGATTACATGGCCTGCCAGCCGAATCCACGGACATGACAAAATA
 TCTGAAAGTGAAACTCGATCCTCCGGATATTACCTGTGGAGACCCCTGAGACGTTCTGTGCAATGGCAATC
 CCTACATGTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCCCTGAGCTGATTTGATT
 GAAGGAAGACATCCCTCACATTGGCAGTCTGCCACTTGGAGGAGTATCCAAGCCTCTCCAGGTTAACAT
 CACTCTGCTTGAGGAAACATTGAGCTAACAGACAACATAGTTACCTTGAATCTGGCGTCCAGACC
 AAATGATCCTGGAGAAGTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTACATGGATCTAAATCCGTGAAGGATTATCACAGCATACCGCTTAGAAATCATTGACACAGA
 AGAGTACTAACAGGGTATAACAACAAATAGCAAATTCACCTTGAAATCAAAGACAGGTTCCGCTTTTG
 CTGGACCTCGCCTACGCAATATGGCTCCCTACGGACAGCTGGATACAACCAAGAAACTCAGAGATTCTT
 ACAGTCACAGACACTGAGGATAAGGCTGTTAAGGACAGCCGTTGGGAAATATTGAGCTACACTGGC
 ACGCTACTTTACCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAAATCTCATGCCACTGTATGT
 TGTATGACAACAGCAAATTGACATGCGAATGTGAGCACAAACACTACAGGTCAGACTGTGGAAATGCAAGAAG
 ATTATCAGGGCGCACCTGGAGTCCAGGCTCTATCTCCCCATCCCCAAGGCAGTCAAATACCTGTATCCC
 CAGTATTTCACTGAGTATTGGTACGAATGTGCGACAACGAGCTCTGCACTGCCAGAACGGAGGGACGTGCCACA
 ACAACGTGCGCTGCCGTGCCGGCGCATACACGGCATTCTGCGAGAACGCTGCCGTGCGAGGAGGCTGGC
 AGCTGCCGTCCGACTCTGGCAGGGCGCCCCCGCACGGCACCCAGCCTGCTGCTGACCACGCTGCT
 GGGACCAGCCCCCTGGTGTCTAGGTGTCACCTCCAGGCCACACGGACGGGCTGTGCCGTGGGAAGCA
 GACACAACCCAAACATTGCTACTAACATAGGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCTAACTGAACTAAGCCATATTATCACCCTGGAGCAGCACATCCGAGTCAAGACTGTTAATT
 TGACTCCAGAGGAGTGGCAGCTGTTGATATTACTGCAAATCACATTGCCAGCTGCAGAGCATATTGGA
 TTGGAAAGGCTGCGACAGCCCCAAACAGGAAAGACAAAAACAAACCAACCGACCTAAAAACATTGGC
 TACTCTAGCGTGGTGCCTAGTACGACTCCGCCAGTGTGGACCAACCAAATAGCATTCTGCTGTCA
 GTGCATTGTGGCATAAGGAAATCTGTTACAAGCTGCCATATTGGCCTGCTCCCTGAATCCCTTCCA
 CTGTCCTTAGTGAACGTTCTGTAACCCCTGTTGGTGAAGATTCTGTTGATGTTAGTGTGACA
 TGTGTAACAGCCCCCTCTAAAGCGCAAGCCAGTCATACCCCTGATATCTAGCAGCACTGAGTCCAGTGC
 GCACACACCCACTATACAAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCCTTTGTATTCAAATGAAGTT
 ATTTCTGTAACACTGTAATATGTAGATTGTTGATTATTGCCAATTGTTGTTACAGACAATCTGTTA
 GTATCTGTAACAGGCAACGAAACGTGCTGGCATCAAAGAATATCAGTTACATATAACAAAGTGTAAAGA
 GATTCTGTAAGGGCAACGAAACGTGCTGGCATCAAAGAATATCAGTTACATATAACAAAGTGTAAAGA
 TTCCACCAAGGACATTCTAAATGTTCTGCTTAACACTGGAAGATTAAAGAATAAAACCTCTGCA
 TAAACGATTCTGAGGATTGCAATTCTTAAGATGAAAGGAACAGCCACCAAGCAGTTCACACTCA
 TTACTGATTCTGTTGACTGAGTACATTGAGTCACTGACGAAATTAGTCCCAGGAAGATGGATTGTTCA
 AGCTTGGACAACCTCTGCAAAATATGAGACTATTCACTGGAAAAATTACAACAGCAAAAAAAA
 AAAAAAA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVGHDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMILEKS LDYGR TWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVDLIRILLRAVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCGKCKNYQGRPSPGSYLPPIP KGTANTCIPSISI GTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLREEAGSCGSDSGQGAPPHTPALLLLTLLGTAS
PLVF

FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCGGTCGGCTAAGATTGCTGAGGAGGC
 CGGGTAGCTGGCAGGCGCCACTTCCGAAGGCCGCGTCCGGCGAGGTGTCCTCATGACTT
 CTCTTGAGGACCATGTCCGTGATCTTTGCCTGCGTGGTACGGTAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTACCACACCCAAGATTTGGAATGGAGGAGACGGCTCA
 AGAGTTAGCCTTGCAGTGGCCCAGTATCCAGGTGAGGTTCTGCAGAACAGTTGTGACTTT
 AGTATAACATTTCTTCTTCGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTCTGCTCCTGGAGACCCTGTGGTGGAAATTACAGCTCCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTCTGAGTTGACAGCATTCA
 AAAGTGAAGTGGCATTAACTATGTAAGTCCCTCTCAGATGGAGTGCAGCTGGAAAAAA
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGTGAATGGCACACACCGATGCACTGGAGCCTGCTCCTAATTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTAACATCATGTGTGCTGCCCTGAATCT
 CATTGAGGAGTTCACCTGCAGAACATTCTTACAGGATCCAAGGAGCTGGTCTGCTGGT
 TGGACCAAACCTCGTGAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTTGATTCTCCAT
 CCGGGAGCAGTGATGTCAAACTCTGCTGCTGGAAATCTCATCAGCAGGGAGCCTGTGGA
 AAAGGGCATGTCAGTGAAATCTGGGAATGGCTGGATTGGAAACATCTGCCATGTGTATTG
 ATGGCAGAGCTGTTGCCACAAGGCCCTTATTAGGGTAAAATTAAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTAACCCTACATTATGATTCTGGGTT
 GCTTCAGAAGTGTATTTCATGAATCATTGATGATTGATCCCCCAGGATTCTATTGT
 TTAATGGGCTTTCTACTAAAGCATAAACTGAGGCTGATTAGTCAGGGCAAAACCAT
 TTACTTTACATATTGTTCAAAACTTGCTGTTCATGTTACACAAGCTTACGGTTTC
 TTGTAACAATAAAATTTGAGTAAATAATGGGTACATTAAACAAACTCAGTAGTACAACC
 TAAACTTGTATAAAAGTGTGAAAAATGTATAGCCATTATCCTATGTATAAATTAAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTATTAAAAA
 AAAAG

FIGURE 76

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFGDVACMAICSCQCPCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVKW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLQTS

FIGURE 77

TGCTTCCTGGAGACCCTGTGGTGGAAATTCACAGCTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTCTTGAGTTGACAGCATCATTAGAAAGTGAAGTGGCATT
TTAACTATGTAAGTCCNTCAGATGGAGTGCAGCTGGAAAAAAATCAGGAGGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

FIGURE 78

CTCAGCGCGCTCCTCGTAGCGAGCCTAGTGGCGGGTGGTGCATTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTAAAACGAGGCAGGGTGGT
 CCTGCCCTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTT
 TCTGTCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTGGCGGGCGGCTT
 CCTCCCCGCTCGTCCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA
TGAAGAACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
 GAGTGTATTATATCAACACCTCTGCAACACTGTACATCCTCTGCCACATCTCCTGAC
 CCGCTTCAAGAACGCTGCTGAGTTACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGACCTTACCCCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCCCTGCCTCGGAACACTACATCCAGTGGCT
 CAACGGCTCCCTCATCCATGGCCTCGGAACCTTGTGTTCTCTCCCCAACCTGTCCTCA
 TCTCCTCATGCCCTTGCAATTCTCACTGAGTCTGAGGGCTTGTGCTCCAGAAAG
 GGTGCTCGGGCCGGGTCTATGAGACAGTGGTGTGATGTCCTCACTCTGCTGGTGCT
 AGGTATGGTGTGGGTGGCATCAGCATTGTGGACAAGAACAGGCCAACAGAGAGTCAC
 ATGACTTTGGGAGTACTATCTCCCTACCTCACTCATGCATCTCCTTGGGTCTG
 CTGCTCTGGTGTGACTCCACTGGGTCTGCCGATGTTCTCCGTCAGGGAAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTAUTGCTCAGCCTTGAGGAGG
 CAGCCCTGACCCGCAGGATCTGTAATCCTACTTCCCTGCTGGCTGCCTTAGACATGGAGCTG
 CTACACAGACAGGCCTGGCTCTGCAGACACAGAGGGCTGCTGGAGAACAGGGCGAACGG
 TTCAGCCTGGCAACGGAACCTGGGTACCCCTGGCTATGCTGTGCTGCTGGTGCTGACGG
 GCCTGTCTGTGCTCATTGGGCCATCCACATCCTGGAGGCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGGCATCAGGGTACCTCCTAGGCCAGGTCTCCTTCCAAGCTGGCTCCTTGG
 TGCCGTCAATTGAGGTACTCATCTTACCTAATGGTGTCTCAGTTGTGGCTTCTATA
 GCTCTCCACTCTCCGGAGCCTGCCAGATGGCACGACACTGCCATGACGAGATAATT
 GGGAACTGTGTCTGCTCTGGCTTAAGCTCAGCACTTCCCTGCTCTCTCGAACCCCTGGG
 GCTCACTCGCTTGACCTGCTGGGTGACTTTGGACGCTCAACTGGCTGGCAATTCTACA
 TTGTGTTCTCTACAACGCAGCCTTGCAAGGCCTCACCACACTCTGCTGGTGAAAGACCTTC
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGCTTGGGCTGGACAGACTGCCGCTGCCGT
 CTCCGGTTCCCCCAGGCATCTAGGAAGACCCAGCACCACTGAAACCTGGGTGGGA
 AGGAAAAAAACTGGACACTGCCATCTGCTGCCCTGGAGGGAGGCCAAGGCTACTTGG
 ACCTCAGGACCTGGAATCTGAGAGGGTGGGCTGGCAGAGGGAGCAGAGCCATCTGCACTATT
 GCATAATCTGAGCCAGAGTTGGGACCAAGGACCTCTGCTTTCCATACCTAACTGTGGCCT
 CAGCATGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCAAATCTGTTACACATCA
 ATCTGCCTCACTGCTGTTCTGGGCATCCCCATGCCATGTTACATGATTGATGTGCAAT
 AGGGTGGGGTAGGGCAGGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGAGATAGATTGTCTCC
 CTTGCCTCTGGCCAGCAGACCTAAGCACTGTGCTATCCTGGAGGGCTTGGACCACCTG
 AAAGACCAAGGGATAGGGAGGAGGCTTCAGCCATCAGCAATAAGTTGATCCCAGGGA
 AAAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKP
IALELCFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFGSRKGVLGRVYETVVMLMLTLLVLMGVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVGFY
SSPLFRSLRPRWHDTAMTQIIGNCVCLVLSSALPVFSRTLGLTRFDLLGDFGRFNWLGNFY
IVFLYNAAFAGLTTLCLVKTAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCAGGNTTCNTCCCC
GCTCGTCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCCGAGTGTA
TTATATCAACACTTCTGTTGCAACACTGTACATCCTCTGCCACATCTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCAAGTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGCAGAGCCTTTAAAACGAGGC GGTTGC
CTGCCCTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGCTGGTGCCTGGCGGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTGCAACACTGTACATCNTCTGCCACATCTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTACCAAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTACCCCTGGCAATTGCCCTGGTGCTGTCCTGCTGCCCTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTGGAGCTGGTGTGCAGTGTCCTGACTGTAAGATCAAGTCCAAACCTGTTT
GGAATTGAGGAAACTCTCTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTC**ATG**CTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCACTGGACAGTTGCAAGGACACCCAGGCCATT
ATTTCCCTCCAGCCTCCATGGACCACAGTCTCCAAGGAGAGAGTGACCCCTACTTGCAA
GGGATTCGCTTCACTCACCAACAGAAAACAAATGGTACCATCGGTACCTTGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTCTCAGAGATGGGATTCC
TCATGCTGCCAGGCTAATGTTGAACCTGGCTCAAGTGATCTGCTCACC**TAG**GCCTCTC
AAAGCGCTGGATTACAGCTCGCTGATCCTGCAAGCTCCACTTCTGTGTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGCAAAGGCGGAAGTAACACTGAATAACTATTACAAGAA
TGATAATGTCCTGGCATTCTTAATAAAAGAACTGACTTCAAAAAAAAAAAAAAAA
AAA

FIGURE 83

MILLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVLTCKGFRFYSPQKTKWYHRYLGKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSEMGFPHAAOANVELLGGSSDLT

FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTCTCGGGACCAGGGAGACCCCCCGGCCCGGGTGT
GAGGCGGCCTCACAGGGCCGGGTGGCTGGCGAGCCGACGCCGGAGGAGGCTGTGAG
GAGTGTGTGGAACAGGACCCGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCACCTTT
GCCTGTTGCTGCTATAACCTCATCGGGCGGTGATTGCCGGACGAGATTCTATAAGATCTTG
GGGGTGCCTCGAAGTGCCTCTATAAAAGGATATTAAAAAGGCCTATAGGAAACTAGCCCTGCA
GCTTCATCCCACCGAACCCCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGGTG
CTGCTTATGAGGTTCTGTCAGATAGTGAGAACGGAAACAGTACGATACTTATGGTGAAGAA
GGATTAAGATGGTCATCAGAGCTCCCATGGAGACATTTCACACTTCTTGGGATTT
TGGTTCATGTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATA
TTATTGTAGATCTAGAAGTCACTTGGAAAGAAGTATATGCAGGAAATTGTTGGAAGTAGTT
AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTCGGCAAGAGAT
GCGGACCAACCCAGCTGGCCCTGGCGCTCCAAATGACCCAGGAGGTGGCTGCGACGAAT
GCCCTAATGTCAAACACTAGTGAATGAAGAACGAAACGCTGGAAGTAGAAATAGACCTGGGTG
AGAGACGGCATGGAGTACCCTTATTGGAGAAGGTGAGCCTCACGTGGATGGGAGCCTGG
AGATTACGGTCCGAATCAAAGTTGTCAAGCACCAATATTGAAAGGAGAGGAGATGATT
TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTGAGATGGATATTACT
CACTGGATGGTCACAAGGTACATATTCCCGGGATAAGATCACCGAGGCCAGGAGCGAAGCT
ATGGAAGAAAGGGAAAGGGCTCCCAACTTGACAACAACAATATCAAGGGCTTTGATAA
TCACCTTGATGTTGAGATTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAA
CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
AATAAAATTGGACTTGTAAATAAGTGAATAAGCGATATTATTCTGCAAGGTTTT
TTGTGTGTGTTTGTAAATTCAATATGCAAGTTAGGCTTAATTGTTATCTAATGA
TCATCATGAAATGAATAAGAGGGCTTAAGAATTGTCATTGCAAGGAAATGACC
AGCAAAAGGTTACTAATACCTCCCTGGGATTAATGTCTGGTGTGCCGCTGAGT
TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
GTTGTTAGCAATTCAAAATGCCAACTGGAGAAGTCTGTTTAAATAACATTGTTG
TTATTTTA

FIGURE 85

MAPQNLSTFCLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLAQLHPDRNPDDPQ
AQEKFQDLGAAYEVLSDEKRKQYDTYGEEGLKDGHQSSHGDFSHFFGDFGMFGGTPRQQ
DRNIPRGSDIIVDLEVTLEEYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVCDECPNVKLVNEERTLEVEIEPGVRDGMEYPFIGEGERPHVDGEPGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD
NNNIKGSLIITFDVDFPKEQLTEEARREGIKQLLKQGSVQKVYNGLQGY

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGAACCCCGGGCCCCCGGTGGAGNGCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCAGGCGGAGGAGGTTTGAGGATTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTGCCTGTTGNTATACTTCATCGGGCGGTGATTGCCGG
ACGAGATTNTATAAGATTTGGGTCCTNGAAGTGCCTNTATAAAGGATATTAAAAAGG
CCTATAGGAAACTAGCCCTGCAGNTTATCCCACCGAACCCCTGATGATCCACAAGCCCAG
GAGAAATTCCAGGATTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAACGGAAACA
GTACGATAATTATGGTGAAGAAGGATTAAAAGATGGTNATCAGAGCTCCATGGAGACATT
TTTCACACTNTTGGGATTTGGTTCATGTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

FIGURE 87

GGCACGAGGCGGCGGGCAGTCGGGATGCGCCGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTGCCACTCCA
 GCAGCTTAGCCCAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGCCACCATCTTCTGGCTTCGTTGCAGCC
 TTGGTGCTGGTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTGTGGACCTCATTGGTGCATGGAGACCCAGTCTGAGCCCTTGAGTTAGAAC
 TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTGAAGATTGTCACACTCTGAC
 AGAGAACGCTTGTGCCATGACAATGGGCTCTGGGCAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCCCTCCGTTGGACCCAAACTCCTGGACGCACGGACTGCCCTGCTCCTGTCAG
 TCACCTGGTGTGGTACAAGGAATGCCATCTGACGGAGGCTGGACTGGATTGACC
 AGTCTCTGTCGGCTGCTGAGGAGCATTGGAAGTCCTCGAGAACGAGCCCTAGCTTGAG
 CCAGATAAAGGCCCTCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATT**TAG**GCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCATCCCTGGATGGCTCAGCTTAGCCTT
 CTACTTTCTATAGAGTTAGTTGCTCCACGGCTGGAGAGTTCAGCTGTGTGCATAG
 TAAAGCAGGAGATCCCCGTCAAGTTATGCCTCTTGCAAGAACGAGCTGGTGGAGT
 GGCAGTCTAATACTACAGTTAGGGAGATGCCATTCACTCTGCAAGAGGGAGTATTGAAAAA
 CTGGTGGACTGTCAGCTTATTTAGCTCACCTAGTGTGTTCAAGAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTCACATTAAAATTAGAATTCTGGCCTCTCGATGGTCAGAATG
 TGTGGCAATTCTGATCTGCATTTAGCAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC
 TTCTTTGGCAAGACTTGTACTCTCACCTGGCCTGTTCAAGGTTATTATTGTATTATCTGCCT
 GGTCCCTGAGCGTCTGGCTCTCCTCTCCCTGCAAGGTTGGTTGAAGCTGAGGAAC
 ACAAAAGTTGATGATTCTTTATCTTATGCCTGCAATTACCTAGCTACCACTAGGTG
 GATAGTAAATTATACCTATGTTCCCTCAAAAAAAAAAAAAAA

FIGURE 88

METVVIVAVGVLATIFLASFAALVLVCRQYCRPRDLLQRYDSKPIVDLIGAMETQSEPS
ELDDVVITNPHEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKT
SASVSDIIVVAKRISPRVDDVVKS MYPPLDPKLLDARTTALLLSVSHLVLVTRNACHLTGGLDWI
DQSLSAAEEHLEVLREAALASEPDKGPGPEGFLQEQSAI

FIGURE 89

GCTTCATTCTCCGACTCAGCTCCCACCTGGCTTCCGAGGTGCTTCGCCGTGCTCC
CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
TTTGGAGTGTTCCTGTTGGAAATGATTCTCTTTGACAAAGCACTACTGGCTAT
TGGAAATGTTTATTGTAGCCGGCTGGCTTGTAATTGGTTAGAAAGAACATTCA
GATCTTCCTCCAAAAACATAAAATGAAAGCTACAGGTTTCTGGGTGGTGTATTGTAGTC
CTTATTGGTGGCCTTGATAGGCATGATCTCGAAATTATGGATTTCTCTGTTCA
GGGCTCTTCCTGTCGGTTATTAGAAGAGTGCCAGTCCTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATAACAACA
AGTGAATTGAAAGACTCATTAAAATATTGTGTTATTATAAAAGTCATTGAAGAATATTCA
GCACAAAATTAAATTACATGAAATAGCTTGTAAATGTTCTTACAGGAGTTAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAAGTGGAGAGGTTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTGAAGGCTATTGTGTTCTTCCACAATGTGCGAAACTCAGCCATCCTAGAGAA
CTGTGGTGCCTGTTCTTTATTGAAAGGCTCAGGAGCATCCATAGGCATTGCT
TTTAGAAGTGTCCACTGCAATGGAAAAATATTCCAGTTGCACTGTATCTGGAAAGTGA
TGCATGAATTGATTGGATTGTGTCATTAAAGTATTAAAACCAAGGAAACCCAATTG
ATGTATGGATTACTTTTGTGNCAGGGCC

FIGURE 90

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFLLFRGFFPVVVGFIIRRVPVLGSLLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTGCCTGGCCTGTTCCCGGCTTCATTCTCCGACTCAGCTTCCC
ACCNTGGGCTTCCGAGGTGCTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTGGAGTGTTTCCTGTCCTTCCA
ATGATTCTCTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTATTGTAGCCGGCTT
GGCTTTGTAATTGGTTAGAAGAACATTCAAGATTCTCTCCAAAAACATAAAATGAAAG
CTACAGGTTTTCTGGGTGGTGTATTGTAGTCCTTATTGGTTGGCCTTGATAGGCATG
ATCTTCGAAATTATGGATTTCTCTTGTTC

FIGURE 92

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTCTGGTTCTAAGTCCATGTGCCAA
 GGCTGCCAGGAAGGAGACGCCTCCTGAGTCCTGGATCTTCTCCTCTGGAAATCTTG
 CTGTGGTAGTTATTATTCTGAATAAGAGCGTCCACGCATC**ATG**GACCTCGCGGACTGC
 TGAAGTCTCAGTCCTGTGCCACCTGGTCTTCTGCTACGTCTTATTGCCTCAGGGCTAATC
 ATCAACACCATTCACTCAGCTCTCACTCTCCTCTGGCCCATTAAACAAGCAGCTCTCCG
 GAA GATCAACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTATGCTGCTGGAGTGGTGG
 CGGGCACCGAATGCACCATCTCACGGACCCCGCGCCTACCTCAAGTATGGAAAGGAAAAT
 GCCATCGGGTTCTCAACCACAAGTTGAAATTGACTTCTGTGTGGCTGGAGCCTGTCCGA
 ACGCTTGGGCTGTTAGGGGCTCCAAGGTCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA
 TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTCGCGCAAGTGGAGCAGGAT
 CGCAAGACGGTTGCCACCAGTTGCAGCACCTCCGGACTACCCGAGAAGTATTTTCC
 GATTCACTGTGAGGGCACACGGTTACGGAGAAGAACATGAGATCAGCATGCAGGTGGCCC
 GGGCCAAGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTCGCCATC
 ACCGTGAGGAGCTTGAGAAATGTAGTTCAGCTGTATATGACTGTACACTCAATTCA
 TAATGAAAATCCAACACTGCTGGGAGTCCTAAACGGAAAGAAATACCATGCAGATTGTATG
 TTAGGAGGATCCCACGGAAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC
 AAGCTTACCAAGGAGAAGGATGCCTTCAGGAGGAGTACTACAGGACGGCACCTCC
 GACGCCATGGTCCCCCGCGGCCCTGGACCCCTCGTAACGGCTGTTGGCCTCG
 TGGTGCTCTACCCCTTCTTCAGTCCTGGTCAAGCTGATCAGGAGCAGGCTTGGCCTCG
 CTGGCCAGCTTCATCCTCGTCTTGTGGCCTCCGTGGAGTTGATGGATGATTGGTGT
 GACGGAAATTGACAAGGGCTGCCTACGGCAACTCTGACAGCAAGCAGAAACTGAATGAC**T**
GACTCAGGGAGGTGTCACCACCGAAGGGAACCTGGGAACTGGTGGCCTCTGCATATCCT
 CCTTAGTGGGACACGGTACAAAGGCTGGGTGAGCCCTGCTGGCACGGCGGAAGTCACGA
 CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGAGGAAGATGTTGTAATCTT
 TTTTCCCCATGTGCTTAGTGGCTTGGTTCTTGTGCGAGTGTGTGAGAATGGC
 TGTGTTGAGTGTGAACCTTGTGATCATAGAAAGGGTATTTAGGCTGCAGGGAG
 GGCAGGGCTGGGACCGAAGGGACAAGTCCCCTTCATCCTTGGTGTGAGTTCTGT
 AACCTGGTTGCCAGAGATAAGTGAAAAGTGTAGGTGAGATGACTAAATTATGCCTC
 CAAGAAAAAAAAATTAAAGTGTGTTCTGGTCAAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLV
MLLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHKFEIDFLCGWSLSERFGLLGGSKVLAKK
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFAITVRSLRVVSAVDCTLNFRNNENPTLLGVNLNGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKFQEEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDS
KQKLND

FIGURE 94

CTGAGGC GGCGGTAGC **ATG** GAGGGGGAGAGTACGT CGGCGGTGCTCTCGGGCTTGCTCG
 GCGCACTCGCTTCAGCACCTAACACAGGACTCGGACACGGAAGGTTCTTCTGGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCAAATGGATGATGTTGAAGTTGTTA
 TACAATTGACATTAGAAATATATTCCATGCTATCAGCTTTAGCTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCCGTCGTATTAGATCAGATCATGACGTTAGAGAGAGGCTGCTTCACAA
 AAACTTGCAGGAGCATTTCAAACCAAGACCTGTTCTGCTATTAACACCAAGTATAA
 TAACAGAAAAGCTGCTACTCATCGACTGGAACATTCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTACTGGTTGCCAATCTGGGATGTCTGAACAACACTGGGTATAAAC
 TGTATCAGGTTCCGTATGTCCACTGGTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTGAAGAAGATGGATCCTAAAGGAGGTACATAAGATAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAAGAGTATATGCAAAAAAGTGGAAAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAACAGATTAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTAGG
 CAGCAAGAGAGAAGAACATCCAAAAGACCCTCAGGAGAACATTTCAGGCATTA
 CGGACCTTTTCAAATTCTGAATTCTCATTCATGTGTTATGTCTTAAAAATAGACA
 TGTTCTAAAGTAGCTGTAACACTAACACCCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCACAAATCTAAC
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTGGTTAGATAACACAAGA
 CAAACGATCTAAAGCAAATCTGGTAGTAGTAACCAAGATAAACGATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAAATTGAAAAGATGAAGGGTTGGTGAATATTACGGCTCCTACA
 TTT**TGA**TCCTTTAACCTTACAAGGAGATTTTATTGGCTGATGGTAAAGCCAAACAT
 TTCTATTGTTTACTATGTTGAGCTACTTGCAGTAAGTCATTGTTACTATGTTCAC
 CTGTTGCAGTAATACACAGATAACTCTTAGTGCATTACTTCACAAAGTACTTTCAAAC
 ATCAGATGCTTTATTCCAAACCTTTTACCTTCACTAAGTTGAGGGAAAGGCT
 TACACAGACACATTCTTAGAATTGGAAAAGTGGAGACCAGGCACAGTGGCTCACACCTGAA
 TCCCAGCACTAGGAAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCAGTCTATTAAAAAATGGAAAAGCAAGAATAGCCTTAT
 TTTCAAAATATGGAAAGAAATTATGAAAATTATGAGTCATTAAATCTCCTTAAG
 TGATACTTTAGAAGTACATTGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTGCAAAACATCATCTAAATTAAAAAAAAAAAAAAAAAAAAA

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLGEVKGEAKNSITDSQMDDVEVVYTIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHE
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSSEQLYKTVSGSC
MSTGFSRAVQTHSSKFFED GSLKEVHKINEMYASLQEELKSICKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVKSS
CNYNHHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDDRWFQKRSRLLDTQDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTE

FIGURE 96

GGCACAGCCGCGCGGGAGGGCAGAGTCAGCGAGCCAGTCCAGCCGACAGCGGACCAGCGCAGGGCAGC
 CCAAGCAGCGCGCAGCGAACGCCGCCGCCACACCCCTCGCGGTCCCCCGCGGCCCTGCCACCCCTCCCT
 CCTTCCCCCGCTCCCCGCCTCGCCGGCCAGTCAGCTGCCGGGTTCGCTGCCCGCGAAACCCCGAGGTACCCA
 GCCCGCGCCTCTGCTTCCCTGGGCCGCGCCCTCACGCCCTCCCTCCGCCCTGGCCCGCCCTGGCACC
 GGGGACCGTTGCCTGACCGAGGCCAGCTACTTTGCCCGCGTCTCTGCCCTGCTGCCCTTCCAC
 CAACTCCAACCTCTTCCCTCAGCTCCACTCGCTAGTCCCCACTCCGCCAGGCCCTGGCCCGCTGCCGTAG
 CGCGCTTCCCCTCCGGTCCCAAAGGTGGAACCGCGTCCGCCCGGCCACCATGGCACGGTTCGGCTTGC
 CGCGCTTCTGCACCCCTGGCAGTGCTCAGCGCCGCGTGTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCG
 AAGTGCACGCTTACGTGTCAAAGGCTCAACAAGAACGATGCCCTCCACGAGATCAACGGTGTATCAT
 TTGAAGATCTGCCCCAGGGTTCTACCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGA
 TGATTCAAAGTGTGGTCAGCGAACAGTGAATCATTGCAAGCTGTCTTGCTTCAAGTTACAAGAAGTTG
 ATGAATTCTCAAAGAACTACTTGAAAATGCAGAGAAATCCCTGAATGATAATGTTGTGAAGACATATGCCAT
 TTATACATGCAAATCTGAGCTATTAAAGATCTTCTGAGTGTGAAACGTTACTACGTGGTGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTGGTGAACTCCCAGT
 ACCACTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT
 CGCAAATTGAAGCTCCAGGTTACTCGTGTCTTGAGCAGGCCGTACTTCGCTCAAGGCTTAGCGGTTGCCGG
 AGATGTCGTGAGCAAGGTCTCCGTAAACCCACAGCCCAGTGTACCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACGCGGGCTCGTACTGTGAAGCCATGTTACAACATGCTCAAACATCATGAGAGGGCTGTTG
 GCCAACCAAGGGATCTGATTGAAATGAAACAAATTCTAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCCTTCAACATTGAATCGGTATGGATCCCATCGATGTGAAGATTCTGATGCTATTATGAACATGCAGG
 ATAATAGTGTCAAGTGTCTCAGAAGGTTCCAGGGATGTGGACCCCCAAGCCCCTCCCAGCTGGACGAATT
 TCTCGTTCCATCTGAAAGTGCCTCAGTGCTCGCTCAGACCCATCACCCCGAGGAACGCCAACACAGC
 AGCTGGCACTAGTTGGACCGACTGGTTACTGATGTCAGGAGAAACTGAAACAGGCCAAGAAATTCTGGTCC
 CCCTTCCGAGCAACGTTGCAACGATGAGAGGATGGCTGCAGGAAACGCCAATGAGGATGACTGTTGGAATGG
 AAAGGCCAAAGCAGGTACCTGTTGCACTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCCAGAGGTCCA
 GTTGACACCAGCAAACCACTGATCCTCGTCAAATCATGGCTTCTCGAGTGATGACCAGCAAGATGA
 AGAATGCATACAATGGGAACGACGTGGACTCTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGGAAAGT
 GGCTGTGAGTATCAGCAGTGCCTCAGAGTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGA
 GAAAGGCCAGTGTGGTGTCCGTCCTGGGCACAGGCCTACCTCCTACTGTTCTGCATCTGTTCC
 TTATGCAGAGAGTGGAGATAAACTCTGAGAAAAAGTGTCAAAAGTTAAAAGGCACCAGTT
 ATCACTTTCTACCATCCTAGTGACTTGTCTTTAAATGAATGGACAACATGTACAGTTTACTATGTGGC
 CACTGGTTAAGAAGTGTGACTTTGTTCTCATTCACTGAGTTGGAGGAAAGGGACTGTGCATTGAGTTGGT
 TCCTGCTCCCCAAACCATGTTAAACAGTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTGTGCATTGTA
 TTTTATCCTCTATTATTGTTGTATGTTCTCATTTGTTGTGGGTTTTTTCAACTGTGATCT
 CGCCTGTTCTTACAAGCAAACCGGGTCCCTTGGCACGTAACATGTACGTTGAAATATTAAATA
 GCTGTACAGAAGCAGGTTTATTATGTTATTAAAAGAAAAAGCCAAAAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKS LNDMF
VKTYGHLIMQNSELFKDLFVELKRYYVVGNVNLEEMLNDFWARLLERMFR LVNSQYHFTDEY
LECVSKYTEQLKPGDVPRKLKLQVTRAFVAARTFAQGLAVAGDVSKVSVNPTAQCTHAL
LKMIYCSHC RGLVTVKPCYNCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKV FQCGPPKPLPAGRISRSISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLKQAKKFWSLPSNCNDERMAAGNGNEDDCWNGKGKSRYLF
AVTGNGLANQGNPPEVQV DTSKPDILILRQIMALRVMTSKMKNAYNGNDVFFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCG**A**TGAAAGTTCTAATCTCTCCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGTCGCCAGAGGCCAC
AGGGACCGAGGCCAGGCTTAGGAGATGGCTCCAGGAAGGCAGGCCAAGAATGTGAGTGC
AGATTGGTTCTGAGAGCCCCGAGAAAGAAAATTCTAGACAGTGTCTGGCTGCCAAAGAAGC
AGTGCCTGATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAGGCACCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTG**T**AGGAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCCACCTCACTCTCCACTGTACCCACC
CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTCAAGATCATTTGTTGCTCTC
TCTAGTGTCTTCTCTCGTCAGTCTAGCCTGTGCCCTCCCTAACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCTAGCTAGTGTCAATTAAACCTTAAATGC
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTAAATGTCAAAAAAAAAAAAAAA

FIGURE 99

MKVLISSLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRKKFMTVSGLPKKQCPDCDFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

FIGURE 100

AATGGCTGTCTTAGTACTCGCCTGACAGTTGTCCTGGACTGCTGTCTTATTCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCTAAGCCTCTGGCACAGAGATCATTGAGAATGCAGTCGA
GTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTATGGAATTGATGATAATGAAGGAA
AACATTCATCAAAGTGACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTCCAGTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAAGGCTCTGGCTTCAACCAACAGAACTCATTGAAACACC
CTGACTGCATTTGCTTTAGAAAGTTAGAATAAAATGGCGCTTGGAATCACATAGTTG
ATGGAGAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 101

MAVLVLRLTVVLLVLFITCYADDKPDKPDDKPDGKDPKPDFPKFLSLLGTEIIENAVE
FILRSMSRSTGFMEFDDNEGHSSK

卷之三

FIGURE 102

GGACGCCAGGCCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTGCCATGGACATCCTGGTCCCACTCCTGCAGCTGCTGGTGTGCTGCTTCTAC
 CCTGCCCTGCACCTCATGGCTCTGCTGGCTGCTGGCAGCCCTGTGCAAAAGCTACTTCC
 CCTACCTGATGCCGTGCTGACTCCAAGAGCAACCGCAAGATGGAGAGCAAGAACGGGAG
 CTCTTCAGCCAGATAAAGGGGTTACAGGAGCCTCCGGAAAGTGGCCTACTGGAGCTGG
 CTGCGGAACCGGAGCCAACTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
 CAAATCCCCACTTGAGAAGTTCTGACAAAGAGCATGGCTGAGAACAGGCACCTCAAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTGTGCTGTGCAGAGCCAAGGAAGGTCTGCAGGGTCC
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTCTGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCCTTCATGTGGCAGCAAGTTTCAGGCCACCTGAAACACATTGGGATGGCTG
 CTGCCTCACCAAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCGAAATCCAAATGG
 AACGACAGCCCCCTCCCTGAAGTGGTACCTGTTGGCCCCACATCATGGAAAGGCTGTC
 AAACAATCTTCCAAGCTCCAAGGCACTATTGCTCCTCCCCAGCCTCCAATTAGAAC
 AGCCACCCACCAGCCTATCTATCTTCACTGAGAGGGACCTAGCAGAACATGAGAGAACATT
 CATGTACCACCTACTAGTCCCTCTCCCCAACCTCTGCCAGGGCAATCTAACTTCATC
 CCGCCTTCGACAGTAAAAAGCTCTACTTCTACGCTGACCCAGGGAGAACACTAGGACCC
 TGTTGTATCCTCAACTGCAAGTTCTGGACTAGTCTCCAACGTTGCCTCCAATGTTGTC
 CCTTCCTCGTCCCAGGTAAAGCTCTCGCTTCCCTGAGGCTACACCCATGCCT
 CTCTAGGAACCTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAACGCCCCCTGACCC
 CTCCCCACTACCACCTCTCCTGAGCTGGGGCACCAAGGGAGAACATCAGAGATGCTGGG
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTGTTCTCAAATATTTTAATAAATAGACGA
 AACCAACG

FIGURE 103

MDILVPLLQLLVLLTLPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQL
KGLTGASGKVALLELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDVVVCTLVLCVQSPRKVLQEVRVLRPGGVLFWEHVAEPYGSWAFM
WQQVFEPTWKHIGDGCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFP
SSKALICSFPSLQLEQATHQPIYLPLRGT

FIGURE 104

GTGGGATTATTTGAGTGCAGATCGTTCTCAGTGGTGGGAAGTTGCCTCATGCAGG
 CAGATGTTGGGCTTGTCCGAACAGCTCCCTCTGCCAGCTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAG**ATG**TCACTCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTACTGGTTGCACCATAACTCCTCAGCTTGAGCAGTTG
 TTAAGGAATGAGGTTACAGATTAGGAATTGTAGGGCCTAACCTATAGACTTTGTCCAAA
 TGCTCTCCGACATGCAGTAGATGGAGACAAGAGGAGATTCCGTGGTCATCGCTGCATCTG
 AAGACAGGCTGGGGGGCCATTGCAGCTATAAACAGCATTAGCACAACACTCGCTCCAAT
 GTGATTTCACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGCCTGGCTAACAG
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCATTGACCCCTAAACTTTGGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTTAACCTTGCAAGGTTCTAC
 TTGCCAATTCTGGTCCCAGCGAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTGCCCTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTCAG
 AAGATTGTGATTGCCTACTAAAGTTGTCATCCGTGGAGCAGGAAACCACTACAATTAC
 ATTGGCTATCTTGACTATAAAAGGAAAGAATTGTAAGCTTCCATGAAAGCCAGCACTG
 CTCATTAAATCCTGGAGTTTGCAACCTGACGGATGAAACGACAGAATATAACTA
 ACCAACTGGAAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCCTGGCT
 GGTAGCATCACAAACACCTCCTCTGCTTATCGTATTTCACAGCACTACCATCGATCC
 TATGTGGAATGTCCGCCACCTGGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTGTAA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTGAAGCCATGGGAAGGACTGCTTCATAT
 ACTGATTTGGAAAAATGGTATATTCCAGACCCAACAGGCAAATTCAACCTAACCGAAG
 ATATAACCGAGATCTCAAACATAAAG**TGA**AACAGAATTGAACTGTAAGCAAGCATTCTCAG
 GAAGTCCTGGAAGATAGCATGGAAAGTAACAGTTGCTAGGCTCAATGCCTATCGGT
 GCAAGCCATGGAAAAGATGTGTCAGCTAGGTAAAGATGACAAACTGCCCTGTGGCAGTC
 AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCCTACCAAGTGT
 ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTCAGCTAGCTGGTACAGA
 TAATTCAAAACTGCTGTTGGTTTAATTGTAAACCTGTGGCCTGATGTAAATAAAACTT
 ACATTTTC

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHHNFLSLSLLRNEVTDSGIVGPQPIDFVPNALRHADGR
QEEIPVIAASEDRLLGGAIAAINSIQHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEPDQGESMKPLTFARFYLPILVPSAKKAIYMDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVVIRGAGNQNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRNITNQLEKWMKLNVEEGLYSRTLAGSITTPPLLIVFYQQHSTIDPMWNVRHLGS
SAGKRYSPQFVKAAKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

FIGURE 106

TGGTTTTGCCCATAAATTCCCTCAGCTTGAGCAGTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGN CCTCAACCTNTAGANTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATT CCTGTGGTCATCGCTGCATNTGAAGACAGGGCTGGGGGGCCAT
TGCAGCTATAAACAGCATT CAGCACAAACACTCGNTCCAATGTGATTCTACATTGTTACTC
TCAACAAATACAGCAGACC ATNTCCGGTCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTGACCTAAACCTTGGAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTAACCTTGCAAGGTTCTACTTGCCAATTCTGGTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTGCCCTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTCAGAAGATTGTGATT CAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCCGGCTGGCTGGCGTAGTGGGCTGCCGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTCAGGGAACGCCAGACAACGGGC
 TGGGCTCCGGGCCTGCAGCGCGCTGAGCTGGCAGGGCGGGCTGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGCCGCGAGCCTTGAGGGAACGACT
 TGTCGGAGCCCTAACCAAGGGGTGTCCTGAGCCTGGGATCCCCGGAGCGTCACATCACT
 TTCCGATCACTCAAAGTGGTAAAAACTAATATTATATGACAGAAGAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGCCTGGCTGTTGCTCTTCTTACTGGTTTGAC
 CATAACTCCTCAGCTGAGGCAGTTGTTAAGGAATGAGGTACAGATTAGGAATTGTA
 GGCCTCAACCTATAGGACTTGTCCAAATGCTCTCGACATGCAGTAGATGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTGGGGGCATTGCAGCTATAA
 ACAGCATTCAAGCACAAACACTCGCTCCAATGTGATTTCTACATTGTTACTCTCAACAAATACA
 GCAGACCATCTCCGGCCTGGCTCAACAGTGATTCCCTGAAAGCATCAGATAACAAATTG
 TCAATTGACCCCTAAACTTGGAAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGAATCC
 ATGAAACCTTAACCTTGCAAGGTTACTTGCAATTCTGGGTTCCAGCGCAAAGAAGG
 CCATATACATGGATGATGTAATTGTGCAAGGTGATATTCTGCCCTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTCAGAAGATTGTGATTGCAGCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTGACTATAAAAGGAAAGAA
 TTCGTAAGCTTCCATGAAAGCCAGCACTTGCTCATTAATCCTGGAGTTTGCAAAAC
 CTGACGGAATGGAAACGACAGAATATAACTAACCAACTGGAAAAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCTGGCTGGTAGCATCACACACCTCTGCTTATCG
 TATTTTATCAACAGCACTTACCATCGATCCTATGTGGAATGTCCGCCACCTGGTTCCAGT
 GCTGGAAAACGATATTCACCTCAGTTGTAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTGGGAAAATGGTATATTCCA
 GACCCAAACAGGCAAATTCAACCTAATCGAAGATATACCGAGATCTCAAACATAAAGTGA
 CAGAATTGAACTGTAAGCAAGCATTCTCAGGAAGTCCTGGAAGATAGCATGCGTGGAAAG
 TAACAGTTGCTAGGCTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTCAGCTAG
 GTAAAGATGACAAACTGCCCTGTCTGGCAGTCAGCTCCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCATTACCAAGTGGTTACTACAATGCTGAATGACTGGAAAGAAGAA
 CTGATATGGCTAGTCAGCTAGCTGGTACAGATAATTCAAAACTGCTGTTGGTTAATT
 GTAACCTGTGGCCTGATCTGAAATAAAACTACATTTCATAGGTAAAAAAAAAAAAAA
 AAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCCTGCCTCGCATGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGCTGCCTGTC**ATG**GGGGCAGCCATCTCCCAGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGCTTCTTGCTGCTGCTCTGGTCATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTGAATCCAGTCCAACCTCAGCCC
TGGCCCCCTGTCCTGAGAAGGCCCCACCACCCAGAACGCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCCCTGGCCTAGCCTGGAGGCCAGGACC**TAA**GTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTAGTGGCCC
TAAGGAGATGGGCCTGGGTGGGGCTTATGAGTTGGTCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCAAGGGCCAAGGGTCAGGGGCCGGTCCACTCTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGCCCCCTCCCTGGTCCTCCAGTGTGCTGGATAATAATGGAACATGGCTCTAA
AAAAAAAAAAAAAAA

109/330

FIGURE 109

MGAAISQGALIAIVCNGLVGFLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRRPHH
PRSPAMKAATCCSPEGPWPSLEPRT

FIGURE 110

GTTTGAATTCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTCCCTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCCTATTCGATCTGTTGATAAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAA
TCATGTGGGAAGAGATAACAATCCTGGCCTGTGTATCCTCGCATTAGCCTGTCTTGGCC
 ATGATGTTACCTCAGATTCATCACCAACCCCTCTGGTTCACATTTCATTTCATTGGTTAT
 TTTGGGATTGTTGTTGTCGCGGTGTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCCTGCTGGGTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGCTCGTCTGATTTGTTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCTTCCAAATCACAAATAAGCCATCAGCAGTGCTCCCTCCTGCTGTTCC
 AGCCACTGTGGACATTGCCATCCTCATTCTCTGGGTCCCTGGTGGCTGTGCTGCTG
 AGCCTGGGAAC TG CAGGAGCTGCCAGGTTATGGAAGGCGCCAAGTGGAAATATAAGCCCCT
 TTCGGGCATT CGGTACATGTGGTGTACCTTAATTGGCCTCATCTGACTAGTGAATTCA
 TCCTTGCCTGCCAGCAAATGACTATAGCTGGGCAGTGGTACTGTTATTCAACAGAAGT
 AAAAATGATCCTCCTGATCATCCCATTCTCGTCTCTCCATTCTCTTCTACCATCA
 AGGAACCGTTGTGAAAGGGCATTAAATCTCTGTGGTGAGGATTCCGAGAATCATTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTCTGGTGTCTGACAAATACCTGCTCCATCTAACCCAGAATGCATA
 TACTACAAC TGCTATTAAATGGGACAGATTCTGTACATCAGCAAAGATGCATTCAAATCT
 TGTCCAAGAACACTCAAGTCACTTACATCTATTAACTGCTTGAGGACTTCATAATTCTA
 GGAAAGGTGTTAGTGGTGTTCACTGTTGGAGGACTCATGGCTTTACTACAATCG
 GGCATTCCAGGTGTGGCAGTCCCTCTGTTATTGGTAGCTTTGCCTACTTAGTAGCCC
 ATAGTTTTATCTGTGTTGAAACTGTGCTGGATGCACCTTCCTGTGTTGTGAT
 CTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTATGGATCAAGAATTCTGAGTT
 CGTAAAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGA
 ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGA**TAG**ATACCCATTAGGTATCTGTACCT
 GGAAAACATTCTAAGAGCCATTACAGAAATAGAAGATGAGACCCTAGAGAAAAGTT
 AGTGAATTTTTTAAAAGACCTAATAAACCCATTCTCCTCAAAA

FIGURE 111

MSGRTIILGLCILALALSLAMMFTFRFITTLLVHIFISLVLGLLFVCGVLWWLYYDYTNDL
SIELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFVFGLMAFNYNRAFQVWAVPLLVAFFAYLVAH
SFLSVFETVLDALFLCAVDLETNDGSEKPYFMDQEFLSFVKRSNKLNNAARAQQDKHSLRN
EEGTELQAIVR

FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTGGACCTCTCCCTGTTCTCCCT
 AGAATAATTGTATGGATTGTGATGCAGGAAAGCCTAACGGAAAAAGAATATTCAATTCTG
 TGTGGTGAAAATTGGAAAAAGGCTTCTCAAACAAGGGTGTCAATTGATATT
TATGAGGACTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCTGTTGCTGG
 TGACTGGAGTACATTCAAACAAAGAAACGGCAAAGAAGATTAAAAGGCCAAGTCACGTG
 CCTCAGATCAACTGCGATGTCAGGCCGAAAGATCATCGATCCTGAGTTCAATTGAAATG
 TCCAGCAGGATGCCAACGACCCAAATACCATGTTATGGCACTGACGTGATGCATCCTACT
 CCAGTGTGTGGCGCTGCCGTACACAGTGGTGTGCTGATAATTCAAGGAGGGAAAATACCT
 GTTCGGAAGGTTGCTGGACAGTCTGGTACAAAGGGAGTTATCCTAACGGTGTCAATCGTT
 ATCCCTACCACGATGGAGAGAATCCTTATCGTTAGAAAAGTAAACCCAAAAGGGTGTAA
 CCTACCCATCAGCTTACACTCATCATCGAAAAGTCCAGCTGCCAACGGCAGGTGAGACC
 AAAAAAGCCTATCAGAGGCCACCTATTCCAGGGACAATGTCACAGCCGGTCACTGTGCA
 GCTTCTGGCTGTCACTGTAGCTGGCCACCCCCACCCCTGCCAACGCCATCCCCTCTG
 CTGCTTCTACCACCAGCATCCCCAGACCAATCAGTGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCACTGCCACCTACACAAGCAGCCAAAACAGGCCAGAGCTGATCCAGGTATCCA
 AAGGCAAGATCCTCAGGAGCTGCCCTCAGAAACCTGTTGGAGCGGATGTCAGCTGGGAC
 TTGTTCCAAAAGAAGAATTGAGCACACAGTCTTGGAGCCAGTATCCCTGGGAGATCCAAC
 TGCAAAATTGACTGCTTTAATTGATGGGAGCACCAGCATTGGCAAACGGGATTCCG
 AATCCAGAAGCAGCTCTGGCTGATGTTGCCAACGCTCTGACATTGGCCCTGCCGGTCCAC
 TGATGGGTGTTGCCAGTATGGAGACAACCTGCTACTCACTTAACCTCAAGACACACACG
 AATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGGAGCTTCTAATGT
 AGGTGGGCCATCTCTTGTGACCAAGAACCTTCTTCAAAAGCCAATGAAACAGAACGG
 GGGCTCCCAATGTGGTGGGTGATGGTGGATGGCTGGCCACGGACAAAGTGGAGGGCT
 TCAAGACTTGCAGAGAGTCAGGAATCAACATTTCTCATCACCATTGAAAGTGCTGCTGA
 AAATGAGAAGCAGTATGTTGGAGGCCAACTTGCAAACAAGGCCGTGTCAGAACAAACG
 GCTTCTACTCGCTCCACGTGCAGAGCTGGTTGCCCTCACAAGACCCCTGCAGCCTCTGGT
 AAGCGGGCTCGCAGACTGACCGCTGCCCTGCAGCAAGACCTGCTGAACCTGGCTGACAT
 TGGCTTCGTCACTCGACGGCTCCAGCAGTGTGGGACGGCAACTTCCGCACCGTCTCCAGT
 TTGTTGACCAACCTCACCAAAGAGTTGAGATTCCGACACGGACACGCGCATGGGGCCGTG
 CAGTACACCTACGAACAGCGGCTGGAGTTGGCTGACAAGTACAGCAGCAAGCCTGACAT
 CCTCAACGCCATCAAGAGGGTGGCTACTGGAGTGGTGGCACAGCACGGGGCTGCCATCA
 ACTTCGCCCTGGAGCAGCTTCAAGAAGTCCAAGCCAAACAGAGGAAGTTAATGATCCTC
 ATCACCGACGGGAGGTCTACGACGACGTCCGGATCCCAGCCATGGCTGCCCATCTGAAGGG
 AGTGTACACCTATGCGATAGGCCTGGCTGGCAAGAGGAGCTAGAAGTCATTGCCA
 CTCACCCGCCAGAGACCACCTCTTGTGGACGAGTTGACAACCTCATCAGTATGTC
 CCCAGGATCATCCAGAACATTGTACAGAGTCACACTCACAGCCTCGAAC**TGA**ATTCAAGAG
 CAGGCAGAGCACCAGCAAGTGTGCTTTACTAAGTGCAGTGTGGACCAACCCACCGCTAA
 TGGGGCACGCACGGTGCATCAAGTCTGGCAGGGCATGGAGAAACAAATGTTGTTATA
 TTCTTGCCATCATGCTTTCATATTCAAACATTGGAGTTACAAAGATGATCACAAACGT
 ATAGAATGAGCCAAAGGCTACATCATGTTGAGGGTGTGGAGATTTCACATTGACAATT
 GTTTCAAAATAATGTTGGAATACAGTGCAGCCCTACGACAGGCTACGTAGAGCTTT
 GTGAGATTAAAGTTGTTATTGATTTGAACTCTGTAACCCCTCAGCAAGTTCAATT
 GTCATGACAATGTAGGAATTGCTGAATTAAAGTTAGAAGGATGAAAAAATAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINC DVKAGKIIDPEFIVKC
PAGCQDPKYH VYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGYSNGVQSL
SLPRWRESFIVLESKP KGV TYP SALTYSSSKSPAAQAGETTKAYQRPIP GTTAQPVTLMQ
LLAVTVAVATPTT LPRPSA ASTTSIPR PQSVGHRSQEMDLWSTATYTSSQNR PRADPGIQ
RQDPSGAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDL SFLIDGSTSIGKRRFR
I QKQLLADVAQAL DIGPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPN VVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGF YSLHVQSWFGLHKT LQPLVKRVCDTDRLACSKTCLNSADI
GFVIDGSSSVGTGNFR TVLQFVTNLKEFEISDT DTRIGAVQYTYEQRLEFGFDKYSSKPDI
LN A I KRVGYWSGGTSTGA A INF A LEQLFKKS KPNKR KLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAWA A QEELEVIATHPARDHSFFVDEF DNLHQYVPRI IQNICTEFNSQPRN

FIGURE 114

CAGGATGAAC TGTTGCAGTGGCTGCTGCTGC GGCGCCTGTGCGCGCTGCCTCAGCACCATGGT
TG CTTCCGGCTGCTCATCCCGCTCGGCCAGATCCGCCACTACAGTTCTCTGACTCTAAT
 GCGCCAGGTCCCACGGCTCCGCCAGATCCGCCACTACAGTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTGGGAATGTCTCAGAATTCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTGATATTGATGTGAACGCCCTGTGTTGAAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGTGGAAGTAGA
 GGCTGGATGCCCTGTTCCGGCCTCCTGAGAATGGCTGAGGAGGCGGCCGAAACACTCC
 TCCCAGCCTTCAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTACTTCATGGCGTG
 AACCCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGACCTTCATTGTTGAATTGC
 CACCCCTGAGCAGCCTCACTGGTACCGCGGTGTTGAAAGATGTGGCCAGAGTGGCTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCAGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
 AAAGTGGGTGGCCCAGGACGCAGGCATCGGGCTGGCGTGGACTCCTACTTGAGTACTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGCCATGTTCTAGAGTATAACAAAG
 CCATCCGGAACTACACCCGCTTCGATGACTGGTACCTGTGGCTCAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTCAGTCCTGGAGGCCTACTGGCTGGCTTCAGAGCCTCATTGG
 AGACATTGACAATGCCATGAGGACCTCCTCAACTACTACACTGTATGGAAGCAGTTGGGG
 GGCTCCCGGAATTCTACACATTCTCAGGGATAACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTTACCGTGCCACGGGGATCCCACCC
 CCTAGAACTCGGAAGAGATGCTGTGGAAATCCATTGAAAAAAATCAGCAAGGTGGAGTGC
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTCCTG
 GCCGAGACTGTGAAATACCTTACCTCTACCTGTTGACCCAACTTCATCCACAACAAATGG
 GTCCACCTCGACCGGTGATCACCCCTATGGGAGTGCATCCTGGGGCTGGGGTACA
 TCTTCAACACAGAACGCTCACCCATCGACCTGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGATTCTACTCTCTCAAACGGAGCAGGTC
 GAAATTCAAGAAAAACACTGTTAGTCGGGCCATGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAAGAAAACATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAAGGTCCA
 CTTCTCAGCTGCCCTCAGTCAGCCCTCACCTCAAGTTGGCATTACTGGGACAGGGTTTCCT
 AGACTCCTCATAACCACTGGATAATTTTATTGAGGCTAAACTATAATA
 AATTGCTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASFETNIRVVGGLLSAHLSSKKAGVEVEAGWPCSGPLLRLMAEEAARKL
LPAFQTPTGMPYGTVNLLHGVPGETPVTCTAGITFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYILWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYYTWKQFG
GLPEFYNI PQGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDNRMESFFLAETVKYLYLLFDPTNFIHNGSTFDAVITYGECEILGAGGY
IFNTEAHPIDLAALHCCQRLKEEWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

FIGURE 116

AAAGTTACATTTCTCTGGAACCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGTTTG
 GGCAGAAAGGAGGGTGCTCGGAGCCGCCCTTCTGAGCTTCTGGGCCGGCTCTAGAACAA
 ATTCAAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAACATGCTTATTTGGAAAGAACAAATGTTCTAGGTCAAACGTGAGTCTACCA
AATGCAGACTTACAATGGTTCTAGAAGAAATCTGGACAAGTCTTCATGTGGTTTTCT
 ACGCATTGATTCCATGTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTAACCAACATGAAGCATCTTGATGTGGAGGCCAGTGATCGCGCCTGGAGA
 AACAGTGTACTATTCTGTCGAATACCAGGGGAGTACGAGAGCCGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTCAGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTAATAGAAACTCAACCACCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGCCCCAGTTGAGTTC
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTCCGAGGAACATGTCAAAATGGTGAGGAGTGG
 GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGCTGCATACTGTGTGAAGGCCAGA
 CATTGTAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAACATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCCTGGTACTGCCCTGTTGCCCTTGTGGCTCATGCTGATCCTGT
 GGTGTCGCACTGTTGTCGGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
 TGTCCTCCCAGACACCTTGAAAATAACCAATTCAACCCAGAAGTTAACAGCTGCAGAAGG
 GAGGAGGTGGATGCCGTGCCACGGCTGTGATGTCTCTGAGGAACCTCCTCAGGGCCTGGAT
 CTCA**TAG**TTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
 ATGAGGGGACAAGTTGTGTTCTGTTTCCGCCACGGACAAGGGATGAGAGAACAGTAGGAAGA
 GCCTGTTGTCACAAGTCTAGAACGCAACCACAGAGGCAGGGTGGTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGAAAAGTGACTTCATCCCTCGGTCTAACGTTCTCATCTGTAATGGGAAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATACACACGTACACATAAA
 TACACCCAGCACTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTGAG
 TGTTCTGGAGAGCAGGACATAATGTATGATGAGAACATGAGACTCTACACACTGGGT
 GGCTTGGAGAGCCCACTTCCCAGAATAATCCTGAGAGAACAGGAATCATGGAGCAATGG
 TGTTGAGTTCACTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTAGCGAGCTACAGT
 AGGTGACCTGGAGGAAGGTACAGGCCACACTGAAAATGGATGTGCATGAACACGGAGGATC
 CATGAACTACTGTAAGTGTGACAGTGTGTCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAACATGCAGAACATGCAAGTCAACATGTGCATGTTGTCCTTTTC
 TGTTGGTAAAGTACAGAACATCAGCAAATAAAAGGGCCACCCCTGGCAAAAGCGGTAAAAAA
 AAAAAAAAAA

FIGURE 117

MQTFTMVLEEIWTSLFMWFYALIPCLLTDEVAILPAPQNLSQLSTNMKHLLWSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTSAW
SILKHPPFNRNSTILTRPGMEITKDFHLVIELEDLGPQFEFLVAYWRREPGAEHHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEQGEAIPLVLALFAFVGMLILV
VVPLFVWKMGRLLQYSCCPVVLPDTLKINTSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGTTGGCAAAAGGAGGTTGCTCGAGCCGCCCTTAGCTT
CCTGGCCGGCTCTAGAACAAATTCAAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTATTTGAAAGAAACAATGTTCTAGG
TCAAACGTGACTACCAAATGCAGACTTCAACATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTCTACGCATTGATTCCATGTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCTCAGAACCTCTGTACTCTCAACCAACATGAAGCATCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCGAATACCAGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCCTCACTCACTGAAGGTCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAAACCTTGTCAGGGCACATTGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGATGGAGATCACAAAGATGGCTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTGAGTTCTGTGGCCTANTGGAGGAGGGCGAACCCCTGCGCGCAAGGG
GTTNGCGAACCCCTTGCAGGCCGCTGGGTATCTCTCGAGAAAAGAGAGGCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTGAGTGGCGCTGGTTGAT

FIGURE 119

CGGACGCGTGGCCGCCACCTCCGAACAAGCC**ATGGTGGCGGCACGGTGGCAGCGCGTG**
GCTGCTCCTGTGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGC GG
TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCTGGTGGTG
AATGTGGCCAGCGAGTGCGGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
AGACCTGGGCCACCACCTTAACGTGCTGCCCTCCCTGCAACCAGTTGGCCAACAGG
AGCCTGACAGCAACAAGGAGATTGAGAGCTTGCCCGCACCTACAGTGTCTATTCCCC
ATGTTAGCAAGATTGCACTGGTACTGGTGCCTCAAGTACCTGGCCCA
GACTTCTGGGAAGGAGCCCACCTGGAACCTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGG
TGGTAGGGCTGGGACCCAACTGTGTCAGTGGAGGAGGTAGACCCCCAGATCACAGCGCTC
GTGAGGAAGCTCATCCTACTGAAGCGAGAACACTTA**TAA**CCACCGCGTCTCCTCCACCA
CCTCATCCGCCACCTGTGTGGGCTGACCAATGCAAACCTAAATGGTGTCAAAGGGAG
AGACCCACTGACTCTCCTCCTTACTCTTATGCCATTGGTCCCATCTTGTGGGGAA
AAATTCTAGTATTTGATTATTGAATCTTACAGCAACAAATAGGAACCTCCTGGCCAATGAG
AGCTCTGACCAGTGAATCACCAGCGATAACGAACGTCTGCCAACAAAATGTGTGGCAA
TAGAAGTATATCAAGCAATAATCTCCACCCAAAGGTTCTGAAACTGGGACCAATGATTAC
CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
CAAATAGGAGGCATTCAATGAACATTGGCATATAAACCAAAAAATAACTGTTATCAAT
AAAAACTTGCATCCAACATGAATTCCAGCCGATGATAATCCAGGCCAACAGTTAGTTGTT
GTTATTCTCTGTATTATTTCTCATTACAAAAGAAATGCAAGTTCAATTGTAACAATCCA
AACAAACCTCACGATATAAAATGAAAGTACCTCCTCAAAA

FIGURE 120

MVAATVAAWLLLWAAACAAQQEQDFYDFKAVNIRGKLVSEKYRGSVSLVVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFCNCQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEVRPQITALVRKLILLKREDL

FIGURE 121

CGGACCGGTGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATGGCTGTCTACGT**CGGGATGC
 TGC~~G~~CTGGGGAGGCTGTGC~~G~~CCGGAGCTCGGGGTGCTGGGGGCCCGCCCTCTCT
 CGGAGTGGCAGGAAGCCAGGGTGCAGGGTGTCCGTTCTCAGTTCCAGAGAGGGTGGATCG
 CATGGTCTCCACGCCATCGGAGGCCAGCTACGTTCAAGGGTGCACCAAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC
 TTGGTCGTCTCCATGAAGACGTCAAGTTGACCTTGCCAACTCAAGGAGGAGGTGGACAA
 AGCTGCTTCTGGCCTCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGCATGTGGGAC
 CTAACTCCTATGCATGGTGCTCATGCAGTTGCCACGCCAGCGGGCATCATCTGGT
 TCTGTGAACCCAGCCTACCAGGCTATGGAACTGGAGTATGTCCTCAAGAAGGTGGCTGCAA
 GCCCTGTGTTCCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCTTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTGC~~C~~GGGACCCTGCTCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGC~~A~~TCTGGACCAGCTCAATACAACCAGCAGTTCTGCTGCCATG
 ACCCCATCAACATCCAGTTCACCTGGGACAACAGGCAGCCCCAAGGGGCCACCCCTCTCC
 CACTACAACATTGTCAACA~~A~~CTCCAACATT~~T~~AGGAGAGC~~G~~CCTGAAACTGCATGAGAAC
 ACCAGAGCAGTTGCGGATGATCCTGCCAACCCCTGTACCATTGCCTGGTTCCGTGGCAG
 GCACAATGATGTCTGATGTACGGTGCCACCTCATCCTGGCCTCTCCATCTCAATGGC
 AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCACCTCCTGTATGGTACCCCCACGAT
 GTTCGTGGACATTCTGAACCAGCCAGACTTCTCCAGTTATGACATCTGACC~~A~~TGTGGAG
 GTGT~~C~~ATTGCTGGT~~CC~~CTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTTGCTTATGGAACCACAGAGAACAGTCCGTGACATT~~CG~~CACTT
 CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGCAGAATTATG~~C~~CTCACACGGAGG
 CCCGGATCATGAACATGGAGG~~C~~AGGGACGCTGGCAAAGCTGAACACGCCGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGCTACTGGGTGAGCCTCAGAAGAACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTCGCCACAATGAATGAGCAGGGCTTGCA
 AGATCGTGGCCGCTCTAAGGATATGATCATCCGGGTGGT~~G~~AGAACATCTACCCGAGAG
 CTCGAGGACTTCTT~~C~~ACACACACC~~G~~AAGGTGCAGGAAGTGCAGGTGGAGTGAAGGA
 CGATCGGATGGGGAAGAGATTG~~G~~CCTGCATTGGCTGAAGGACGGGAGGAGACCACGG
 TGGAGGAGATAAAAGCTTCTGCAAAGGGAAAGATCTCAACTCAAGATTCCGAAGTACATC
 GTGTTGTCACAAACTACCCCTCACCATT~~C~~AGGAAAGATCCAGAAATTCAAAC~~T~~CGAGA
 GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGCAGGCC~~T~~GT~~C~~CTGGCCGGTTGGCTT
 GACTCTCTCTGTCAGAATGCAACCTGGTTATGCACCTAGATGTCCCAGCACCCAGTT
 TGAGCCAGGCACATCAAATGTCAAGGAATTGACTGAACGA~~A~~CTAAGAGCTCCTGGATGGTC
 CGGGAACTCGCCTGGCACAAGGTGCCAAAGGCAGGCAGC~~T~~GCCAGGCC~~T~~CCCTCCTG
 TCCATCCCCACATTCCCTGTCTG~~C~~TTGTGATTGGATAAAAGAGCTTCTGTTTCTT
 GAAAAA

FIGURE 122

MAVYVGMLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRLFSSREVDRMVSTPIGGLSYVQ
 GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRLPDLTAVISVDAPLPGTLLIDEVVAAGSTRQHLDQLQYN
 QQFLSCHDPINIQFTSGTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPVTFAHFPEDTVEQKAESVG
 RIMPHTEARIMNMEAGTLAKLNTPGELECIRGYCVMLGYWGEPKTEEAVDQDKWYWTGDVAT
 MNEQGFCKIVGRSKDMIIRGGENIYPAELEDFFHTHPKVQEJVQVVGVKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413**N-glycosylation Site:**

amino acids 282-285

FIGURE 123

CAACTCCAACATTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCCTCATCCTGCCCTCTCCATCTTCAATGGCAAGAAGGCACGGAGGC
CATCAGCAGAGAGAGAGAGGACCTTCCTGTATGGTACCCCCACGATGTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTGACCATGTGTGGAGGTGTCAATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCC GTGACATT CGCG CACT CCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGCTACTGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

FIGURE 124

GAGCAGGACGGAGCCATGACCCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCACGGACAATTCTGCTGGC
 AGTGCGGGTTGCGGTTGGACTCCCCGGCAAGAATGACCGGGCTGGATCTCACGGGC
 TTCTGGCGTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCAACCGGCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGCCTGAGCCGGAGGCAGGGTACATGCCGCCGGTCGTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTCGACGCCAACGTACCTGACGGCA
 GCTAATGTGACTGTGTCCTGCCTGTCCGGGCTGTGTCCAGGATGAATTCTGCACTCGGG
 TGGAGTAACAGGCCAGGGTTACGCTCAGTGGCTCCTGTTGCCAGGGTCCCCTGTAAC
 CTGACCTCCGCAACAAGACCTACTTCTCCCCCTGAATCCCACCCCTTGTCCGGCTGCCCC
 CCAGAGCCCACGACTGTGGCCTAACCATCTGTCAACCACACTTCTACCTCGGCCAGTGAG
 ACCCACATCCACCAACCCATGCCAGGCCAACCAAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCTCCGGATGAGGAGCCCAGGTTGACTGGAGGCCGCTGGCCACCAGGAC
 CGCAGCAATTCAAGGGCAGTATCCTGCAAAAGGGGGCCCAAGCAGCCCCATAATAAGGCTG
 TGTGGCTCCCACAGCTGGATTGGCAGCCCTCTGTTGCCGTGGCTGCTGGTGTCTACTGT
GAGCTTCTCCACCTGAAATTCCCTCTCACCTACTTCTGCCCTGGTACCCCTTTCT
 CATCACTCCTGTTCCCACCACTGGACTGGCTGGCCAGCCCCCTGTTTCAACATTCCC
 CAGTATCCCCAGCTTCTGCGCTGGTTGCGGCTTGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTGAGGACAGCTCCTGTATCCTCTCATCCTGTCTC
 TCCGCTTGTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGAAGGTG
 AGAGAGAGGATGCTAAGCTCCTACTCACTTCTCCTAGCCAGCCTGGACTTGGAGCGTGG
 GGTGGGTGGACAAATGGCTCCCCACTCTAACGACTGCCTCCCTACTCCCCGCATTTGGG
 GAATCGGTTCCCCATATGTCTCCTACTAGACTGTGAGCTCCTCGAGGGGGGCCGGTAC
 CCAATTGCCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLRLGGAQALECYSCVQKADDGSPNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAIFIQLQQCAQDRCNAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPVVSCYNASDHVYKGCFDGNVTLTAANVTV
SLPVVRGCVQDEFCTRDTGVTGPGFTLSGCCQGSRCNSDLRNKYFSPRIPIPPLVRLPPPEPTT
VASTTSVTTSTSAPVRPTSTTKPMPAPTSQTPRQGVEHEASRDEEPRLTGGAAGHQDRSNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

FIGURE 126

CGGGACTCGCGGGTCTCCTGGAGTCTGGAGGGACGGCTGTGCAGACGCC**ATGG**GAGT
 TGGTGCTGGTCTTCCTCTGCAGCCTGCTGGCCCCATGGCCTGGCCAGTGCAGCTGAAAAG
 GAGAAGGAAATGGACCCTTTCAATTATGATTACCAGACCTGAGGATTGGGGACTGGTGT
 CGCTGTGGCCTCTCGGTTGGATCCTCCTTATCCTAACGTCGAGGTGCAAGTGCAGTT
 TCAATCAGAACAGCCCCGGGCCCCAGGAGATGAGGAAGCCCAGGTGGAGAACCTCATCACCGCC
 AATGCAACAGAGCCCCAGAACGAGAACACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAA
 CCTGAGGCAGCTGCTGAACCTTGGATGCAAATGTCGATGCT**TAA**AAAACCGGCCACTTC
 AGCAACAGCCCTTCCCCAGGAGAACCCAAGAACCTGTGTGCCCCACCCATCCCCCTCTA
 ACACCATTCCACCTGATGATGCAACTAACACTTGCCTCCCCACTGCAGCCTGCGGTCT
 GCCCACCTCCCGTGTGTGTGTGTGTGTGACTGTGTGTTGCTAACTGTG
 GTCTTGTGGCTACTTGTGTGGATGGTATTGTGTTAGTGAACGTGGACTCGCTT
 CCCAGGCAGGGCTGAGCCACATGCCATCTGCTCCTCCCTGCCCCCTGGCCCTCCATCAC
 CTTCTGCTCCTAGGAGGCTGCTTGGCCAGACCAGCCCCCTCCCTGATTTAGGGATGC
 GTAGGGTAAGAGCACGGGCAGTGGCTTCAGTCGTTGGACCTGGGAAGGTTGCAGCAC
 TTTGTATCATTCTCATGGACTCCTTCACTCCTTAACAAAAACCTGCTTCCTTATCCC
 ACCTGATCCCAGTCTGAAGGTCTTAGCAACTGGAGATAAAAGCAAGGAGCTGGTGGCC
 CAGCGTTGACGTCAAGGCAGGCTATGCCCTCCGTGGTTAATTCTCCAGGGCTTCCACG
 AGGAGTCCCCATCTGCCCGCCCTCACAGAGGCCGGGATTCCAGGCCAGGGCTTCT
 ACTCTGCCCTGGGAATGTGTCCCCCTGCATATCTCTCAGCAATAACTCCATGGCTCTGG
 GACCCTACCCCTCCAACCTTCCCTGCTTGTGAGACTCAATCTACAGGCCAGCTCATCCAG
 ATGCAGACTACAGTCCCTGCAATTGGGTCTGGCAGGCAATAGTTGAAGGACTCCTGTTCC
 GTTGGGCCAGCACACCGGATGGATGGAGGGAGAGCAGAGGCCCTTGCTTCTGCCTACG
 TCCCCTTAGATGGCAGCAGAGGCAACTCCGCATCCTTGCTCTGCCTGTCGGTGGTCAGA
 GCGGTGAGCGAGGTGGGTTGGAGACTCAGCAGGCTCCGTGCAGCCCTGGAACAGTGAGAG
 GTTGAAGGTATAACGAGAGTGGAACTCAACCCAGATCCGCCCTCCTGCTCTGTGTT
 CCCGCCAAACCAACCAACCGTGCCTGTGACCCATTGCTGTTCTGTATCGTATCTAT
 CCTCAACAACACAGAAAAAGGAATAAAATATCCTTGTTCCT

FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHVDYQTLRIGGLVFAVVLFSVGILLILSRRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTEVQPSGGSLWNLRLLEPLDANVDA

FIGURE 128

AAACTTGACGCCATGAAGATCCCGGTCTTCCCTGCCGTGGTGCTCCTCTCCCTCTGGTGCT
CCACTCTGCCAGGGAGCCACCCTGGGTGGTCTGAGGAAGAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTAACACCCCCTGAACTCGACAAATTGCGATCTGCGTT
AAGGCTGATGAGTTCTGAACGGCACGCCCTTTGAGTCTATCAAAAGGAAACTCCTT
CCTCAACTGGGATGCCTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCAGT
GACCATGACCTCCACTGGAAGAGGGGGTAGCGTGAGCGCTGATTCTAACCTACCATAACT
CTTCCTGCCTCAGGAACTCCAATAAAACATTTCCATCCAAA

FIGURE 129

MKIPVLPAVVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSAFKADE
FLNWHALFESIKRKLPFLNWDAFPKLKGLRSATPDAQ

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTAGGAATACAAACCAGCC**ATG**GGGTGGAGATTGC
CTTGCCCTCAGT GATTCTCACCTGCCTCTCCCTCTGGCAGCAGGAGTCTCCCAGGTTGTC
TTCTCCAGCCAGTCCA ACTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGC CGGCCACTCA**TGA**GAGTGT TGTAAAGTATTTTAGAATACTGTTGACTTCT
TCATGATTAATAACCATCCTTGCAGTTTATGAGGCTTAGGGGAATGTCAACCCTCA
AATTTTGT TATACTAGATGGCTTCCATTACCCACCACTATTTAAGGTCCCTTATTTT
AGGTTCAAGGTTCATTTGACTTGAGAAAAGTGCCTCTGCAGCTCATTGATTTGTTATC
TTCACTATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATT
TATCCCTGGGTGCCCTGACACATTATGTAGTGATCCCACAAATGTGATTGTTAATTAAA
TGTTATTCTAATATTAGTACATT CAGTTGTGATGTAATATGAATAACCAGAATCTATTCTT
AAAAGTTTGAGTATTTCAACTAGATATTGTATAGAAAGACTGAATAGTGATG

FIGURE 131

MGVEIAFASVILTCLSLLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGGCG**ATG**GAGTGGTGGGCTAGCTGCCGCTCGGCTCTG
 GCTGCTGTTGTTCCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
 AAGTATTTATTGACCAAATTAAACAGGTCTTGAGAATTACGAACCATGTTCAAGTCAAAC
 TGCAGCTGCTACCATGGTGTAGAAGAGGATCTAACCTCCTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACAAGAAC
 GACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTATT
 TTGGAAGTGATCGGGCGTCCCTGACATGGAGATGGTGTCAATGTACGAGATTACCTCA
 GGTTCCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTGGACATTTGGAAAGGGGACCTGCTGTTGGCCAATTTAT
 CCTACAGGTCTGGACGGTGGGACCTCTTCAGAGAAGATCTGTAAGGTCAAGCACAGTG
 GCCATGGAAAAAGAAAAACTCTACAGCATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTCTGTCTCGAAAAACCCAAAATTGTTGATGCAGAAATACACCAAAAC
 CAGGCCTGGAAATCTATGAAAGATACTTAGGAAAGCCAGCTGCTAAGGATGTCCATTTGT
 GGATCACTGCAAATACAAGTATCTGTTAATTCGAGGCGTAGCTGCAAGTTCCGGTTA
 AACACCTCTCCTGTGGCTCACTGTTCCATGTTGGTAGCTGGCTAGAATTCTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTGTAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGAA
 GCCAGTTATTAGGAACCATTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTG
 AGTGAATACTCTAAATTCTGTCTTATAATGTAACGAGAAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAAATGAACT**TAG**TAGTCATCATAGGACCATAGCCTCTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAGCTGGCTCCTATACCTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTCTTATCATGCTGCACCCAGAGCAACTCTGAGA
 AAGATTAAAATGTTCTAATACACTGATATGAAGCAGTTCAACTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTGAACCCAACTCTACCTTCACTGGTAGTCAAGGAAATC
 ACAGCTTGTGCCTCAGATCATCCACCTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTGTCCATTATTGGAGCAGAAAATTGTCATTGGAGTACAA
 CTCATTGCTGGAATTGTGAAATTATTCAAGGCAGTCTGTCACTTTATTAAATGTAGG
 AAACCCATTGGGTTATGAAAAATCTGGGATCATTCTCTGAATGGCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTGTAAAACCATAAAACTCTGTTACTCAG
 GAGGTTCTATAATGCCACATAGAAAGAGGCCATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTGTGCCCTCATGCCCTACTTCTTAATGCCCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLPSAQGRQKESGSKWKVFIQINRSLENYEPCSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT
LKGPAAKDVHLVDHCKYKLFNFRGVAASFRFKHLFLCGSLVFHVGDREWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY
NVTRRKGYDQIIPKMLKTEL

FIGURE 134

CACCCCTCCATTCTGCCATGGCCCCTGCACTGCTCCTGATCCCTGCTGCCCTGCCTCTT
 TCATCCTGGCCTTGGCACCGGAGTGGAGTTCGTGCCTTACCTCCCTCGGCCACTTCTT
 GGAGGGATCCGGAGTCTGGTGGTCCGGATGCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATTGCCCCCTGGCATGGATCTGGGCTCCTGCTCTATTGTTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTGGGTCCCTCAG
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCAGCTGGTATGCGGTACTGGGAGCC
 CATAACCAAAGGCCCTGTGTTGGAGGCTGGGCTGAGCCATGGCACCTGGGTGCCGC
 TCCTCTGCTTGCTCCATGTCATCTCCTGGCTCCTCATCTTAGCATCCTCTCGTCTT
 GACTATGCTGAGCTCATGGCCTCAAACAGGTATACTACCATGTGCTGGGCTGGCGAGCC
 TCTGGCCTGAAGTCTCCCCGGCTCTCAGACTCTCTCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGCTGTGGTGGTGCCTACCCCTGGCACGGACCGTCTCCTTGCT
 TTCCTCCTTACCCCTACCTGGCCTGGCTCACGGCTTGATCAGCAAGACCTCCGCTACCT
 CGGGCCCAGCTACAAAGAAAATCCACCTGCTCTCGGCCAGGATGGGAGGCAGAGT
GAGGAGCTCACTTGTTACAAGCCCTGTTCTCCTCTCCACTGAATTCTAAATCCTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTTATTCTCTGGTCCAGCTCCATACCCTAAATTCTGAGTTCAGCCA
 CTGAACCTCCAAGGTCCACTCTCACCAAGGAAGAGTGGGTATGGAAGTCATCTGCC
 TTCACTGTTAGAGCATGACACTCTCCCCCTCAACAGCCTCTGAGAAGGAAAGGATCTGCC
 CTGACCACCTCCCTGGCACTGTTACTGCCTCTGCCCTCAGGGTCCCTCTGCACCGCT
 GGCTTCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGCCCTCCA
 GGCCCCAACCTGCCTCACCACTCCGGCCCTAGTCTCTGCACCTCTTAGGCCCTGCCTCT
 GGGCTCAGACCCAACCTAGTCAAGGGATTCTCCTGCTCTTAACTCGATGACTGGGCTC
 CCTGCTCTCCGAGGAAGATGCTCTGCAGGAAAATAAGTCAGCCTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILA FGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLL FVGQHSLMAAERVKA WTSRYFGV IQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAE PWATWVPLL CFVLHV ISWLLI FSILLVFDY AELMGLKQVYYHVLGLGEPLALKSP
RALRLFSHLRHPVCVELLTVLWVVPTLGD RLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDG EAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCTGCCTTAGGAGGTGGCTGCCTGGAAAAGCTATCAAGGA
 AGAAATTGCCAACCATGTCTTTCTGTTTCAGAGTAGTCACAACAGATCTGAGTGT
 TTTAATTAAGCATGGAATACAGAAAACAACAAAAACTTAAGCTTAATTCATCTGGAATT
 CCACAGTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTCCCGCTGGCTGCTCTA
 TCACGTGGTGCTCTCGACTACTCACCCCGAGTGTAAAGAACCTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGG**ATG**GCCTCGGCTCTGGACTGTCCTCCGAGTAGGATGTCACTGAGATCC
 CTCAAATGGAGCCTCCTGCTGTCACTCCTGAGTTCTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACCGCGTGAACGGATGTACTTCTATGAGTATGAGCCGATT
 ACAGACAAGACTTCACTCACACTCGAGAGCATTCAAACGTCTCATCAAATCCATT
 CTGGTCATTCTGGTACCTCCCACCCCTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAGGAAAGTCTGGTGGGATATGAGGTTCTTACATTTCTTATTAGGCCAAG
 AGGCTGAAAGGAAGACAAAATGTTGGCATTGTCCTTAGAGGATGAACACCTCTTATGGT
 GACATAATCCGACAAGATTTTAGACACATATAAACCTGACCTGAAAACCATTATGGC
 ATTCAAGGTGGTAACTGAGTTGCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTAGTGAAGTATCTTAAACCTAAACCACTCAGAGAAGTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCCTATAGAGGATTTACCAAAAAACCCATAT
 TTCTTACCAAGGAGTATCCTTCAAGGTGTTCCCTCCACTGCAGTGGTTGGTTATATAA
 TGTCCAGAGATTGGTGCCAAGGATCTATGAAATGATGGTCACGTAAAACCCATCAAGTT
 GAAGATGTTATGTCGGGATCTGTTGAATTATTAAAAGTGAACATTCAATTCCAGAAGA
 CACAAATCTTCTTCTATAGAACATTGGATGTCTGTAACTGAGACGTGATTG
 CAGCCCATGGCTTCTTCAAGGAGATCATCACTTTGGCAGGTATGCTAAGGAACACC
 ACATGCCATTAT**TAA**CTTCACATTCTACAAAAGCCTAGAAGGACAGGATACCTGTGGAAA
 GTGTTAAATAAAAGTAGGTACTGTGGAAAATTCAATGGGGAGGTCACTGCTGGCTTACACTG
 AACTGAAACTCATGAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTATTAGTC
 AGGCCCTCAAAGATGATATGTGGAGGAATTAAATATAAGGAATTGGAGGTTTGCTAAA
 GAAATTAAATAGGACCAACAATTGGACATGTCATTCTGTAGACTAGAATTCTAAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAACAAAACAATGTAGAGTTATTATTG
 AACAAATGTAGTCACTGAGGTTGTATATCTTATGTGGATTACCAATTAAAATATA
 TGTAGTTCTGTGTCAAAAACTTCACTGAAGTTACTGAACAAAATTACCTGTGTTT
 TGGTCATTATAAAAGTACTTCAAGATGTTGCAGTATTCACAGTTATTATTATTAATTA
 CTTCAACTTGTGTTTAAATGTTGACGATTCAATACAAGATAAAAAGGATAGTGAAT
 CATTCTTACATGCAAACATTCCAGTTACTTAACGATCAGTTATTATTGATACATCAC
 TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTGGACTTGTAAAT
 ATTTTACTGTGGTAATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPIYRQDFHFTLREHSNC SHQNPFVLVLTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFFLLGQEAEKEDKMLALSLEDEHLLYGDIIHQDFLDTYNNLTLKTIAMFRWVTEFCPNAKYVMKTDTDVFIN TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRITHLDVCQLRRVIAAHFSSKEIITFWQVMLRNTTCHY

卷之三

FIGURE 138

CCTCTGTCCACTGCTTCGTGAAGACAAG**ATG**AAGTTCACAAATTGTCTTGCTGGACTTCTT
GGAGTCTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAAATGTGGCCAATGTTGACA
ATAACAAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGAAATGGCTTGCTGCAACC
AGACTCTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCACCCAAACAAAGTCGATGACCTGAGCAAGTCGGA
AAAAACATTGCAAACATGTGCGTGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGGACATT
CCTTCTGTGGAGACACGGTGGAGAAC**TAA**ACAATTAAAGCCACTATGGATTAGTCAT
CTGAATATGCTGTGCAGAAAAATATGGCTCCAGTGGTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTGATTTCTTAAGTTCAATAAAATCATTAGCATTGAAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVVNNEHNVANVDNNNGWDSWNS
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSTIQSLDALVKEKKLQGKGPGGPPPGLMYSVN
PNKVDDLSKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

FIGURE 140

CATTTCTGAAACTAATCGTGTCAAGATTGACTTGAAAGCATTGCTTTACAGAAGTATA
 TTAACCTTTAGGAGTAATTCTAGTTGGATTGTAATATGAAATAATTAAAAGGGCTTCG
 CTCATATATAGGAAAATCGCATATGGCCTAGTATTAAATTCTATTGCTTACTGATTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTATGTAAGCTTCAGAAGAACTGGTTGTTACATG
 CAAGCTTATAGTTGAAATATTTTCAAGGAAATTAC**ATG**AATGACAGTCTCGAACCAATGTGT
 TTGTTGATTCACCAGAGACTATGCATGTGCTTGCATCTACCTGCAGCTAGAGCACCT
 CAGATTCCGTTGCCAACTCGTCCCCATTGGTTCTCTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTATACCAGAAAAAGCCAAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTAAAAGCAAAGGGA
 TTGAATCCGGATGGAACCTCCAGCCCTTCAACCCTGGTGGATTTCTCCAGCCTCCAAGCC
 ATCATCACCAAGAGAAGTAAAGCTGAAGAGAAATCCAATCTCCATTAAATGTGAAGACAG
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTCCAAAAGCCCTACAATGGTGTAAAGAAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATATCAT
 GGTTCTCCTCACCTTAAGGCCAAGCATAACCAGAGATGATTAAAAAGTCAAACAGACATGG
 TCATAAAAGGAAAAATCTGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAACACAGGCATGAAAGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTT
 GAGAGGTCCCATAAAAGCAAGCACCAGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
C**TGA**CTTTCTCTCCTTGAGCCTGCATCAGTTGGTTGCCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAACATTAAACGCAAACGTGATTAGGATTGATTCTTGAAACCCCTCA
 GGTCTCTAGAACACTGAGGACAGTTCTTGAAAGAAACTATGTTAATTGGTACATTGACATT
 AAAATGCCCTAGCAGTATCTAATTAAAAACCATGGTCAGGTTCAATTGTACTTTATTAGT
 TGTGTATTGTTATTGCTATAAGAACTGGAGCGTGAATTCTGTTAAAGTGTATCTTATT
 ATACAGATAAAATTGAGACACTGTTCTATTAAAGTGGTTATTGTTAAATGATGGTGAAT
 ACTTTCTTAACACTGGTTGTGCATGTGTAAAGATTACAAGGAAATAAAACAAAT
 CTTGTTTTCTAAAAAAAAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWFLLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFPASKPSSPREVKAEEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTRSRSSHTPRRHYN
NRRSRSGTYSSRSRSRSRSHSESPRRHNNHGSPHLKAKHTRDDLKSSNRGHKRKKRSRSQ
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRGHGRHRR

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTAAAGATTATTGGAAGGGGTTATCA
TTTTTGAAANNTATCGGGTCANAATTGNCTTGAAAAGCATTGCTTTTACAGAAATATAT
TANCTTTTAGAGTAATTCTAGTTGGATTGTAATATGAAATTATTTAAAAGGGCTCGCT
CATATATAGGAAAATCGCATATGGCCTAGTATTAAATTNTTATTGCTACTGATTTTTG
AGTTAAGAGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAAGTAGATTGAGTCTCCAATTTATGTAAGCTCAGAAGAACTGGTTGTTACATGCA
AGCTTATAGTTGAAATATTTTCAAGGAATTACATGAATGACAGTCTCGAACCAATGTGTT
GTTCGATTCAACCAGAGANTATGCATGTGCTTGCATCTACCTGCAGNTAGACACTTCA
GATTCCGTTGCCAACTNGTCCCCATTGGTTCTTCTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTATACCAAGAAAAAGCCAAACTATGAATTACTG
AAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTACAAGAAGCCNAATTAAAAGCAAAGGGATT
GAATCCGGATGGAACTCCAGCCCTTCAACCCTGGGTGGATTCTCC

FIGURE 143

GGCACGAGGCCTCGCCAAGCTGGCACGAGGGTGACCGCGTTCTGCACGCGTC**ATGGC**
 GGTCTCGGAGTACAGCTGGTGGTACCCCTGCTCACTGCCACCCATGCACAGGCTGGCGC
 CACACTGCTCCTCGCGCTGGCTCTGTAACGGCAGTTGTTCCGATAACAAGCACCCG
 TCTGAGGAGGAGCTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
 GGCAATGGCCTAGTGAGGAGAACCGACTGTCTGTCCCCGAGATGCCCGTCCAGCTGG
 AGACCTGCCCTCACGACCGTGGATGCCCTGGCCTGCGCTTCTTGGAGTACCGAGTGG
 TTTGTGGACTTGCTGTACTCGGGCGCGTGTACCTCTCACAGAGGCCTACTACTACAT
 GCTGGGACCAAGGAGACTAACATTGCTGTGTTGGTGCCTGCTCACGGTACCTCT
 CCATCAAGATGTTCCCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGTGAGCGC
 TCTGTCTGCCTCACCTTGCTTCCTCTGCTGGCATGCTGGTCAAGTGGTGC
 GGAGGAGACCCTCGAGCTGGCCTGGAGCCTGGCTGCCAGCATGACCCAGAACTTAGAGC
 CACTTCTGAAGAACGAGGGCTGGACTGGCGCTTCCGTGGCCAAGCTGGTATCCGCGTG
 GGACTGGCAGTGGTGGCTCTGTGCTGGTGCCTCCTCACCTCCCAGGCCTGCGGCTGG
 CCAGACCCACCGGGACGCACTGACCATGTCGGAGGACAGACCCATGCTGAGTCCCTCTGC
 ACACCAGCTTCCCTGTCCTCCCTGTTCATCCTGTGGCTCTGGACAAAGCCCATTGCACGGAC
 TTCCTGCACCAGCCGCCCTGGGAGACCGCTGGCTCCCTGCTGTCCGATTCTGCCTCGA
 CTCTGGCGCCTCTGGTGGCTGTGCTGCCCTGCTGCCGCTGGCGGTGACCCGGCCCC
 ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
 CGCATCGAAGCCCGTGAATCCAGCAGAGGGTGGCTCGAGTCTACTGCTATGTGACCGTGGT
 GAGCTTGCAGTACCTGACGCCGCTCATCCTCACCCCTCAACTGCACACTCTGCTCAAGACGC
 TGGGAGGCTATT CCTGGGCCCTGGGCCAGCTCCTCTACTATCCCCGACCCATTCTCAGCC
 AGCGCTGCCCATCGGCTCTGGGAGGACGAAGTCCAGCAGACTGCAGCGCGATTGCCGG
 GCCCTGGTGGCCTGCTACTCCCTCTCCGTGGCGTCTGGCCTACCTCATCTGGT
 GGACGGCTGCCAGCTGCTGCCAGCCTTGGCCTCTACTCCACCAAGCACTGGCA
 GGCTCC**TAG**CTGCCTGCAGACCCCTCTGGGCCCTGAGGTCTGTTCTGGGCCAGCGGGACA
 CTAGCCTGCCCTCTGTTGCCTGGGCCCTGAGGTCTGCAAGGTGGGCCGGACTCCCC
 GGCGTTCCCTCACCAAGTGCCTGACCCGCCCTTGGACGCCAGTGTCCGAAGCGTATG
 GAGCTCTCTGGGCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCCGAAGCGTATG
 TGCCAGGTTGAGTGGCGAGGGTGATGCTGGCTGCTTCTGAACAAATAAGGAGCATGCC
 GATTTTAA

FIGURE 144

MAVLGVQLVVTLITATLMHRLAPHCSFARWLLCNGSLFRYKHPSEEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPPLTTDALVLRFFLEYQWFVDFAVYSGGVYLFTTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGGERSVCLTF AFLFLLLAMLVQV
VREETLELGLEPGLASMTQNLEPLLKKQGWDWALPVAKLAIRVGLAVVGSVLGAFLT FPGLR
LAQTHRDALTMS EDRPMLQFLLHTSFLSPFILWLWTKPIARDFLHQPPFGETRF SLLSDSA
FD SGRLWLLVVLCLLRLAVTRPHLQAYLCI AKARVEQLR REAGRIEAREIQQRVVRVYCYVT
VVSLQYLTP LILT LNCTLLKTLGGYSWGLGPAPLLSPDPSSASA API GSGEDEVQQTAARI
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLF GLYFH QHLAGS

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCCTCGGAGTACAGCTGGTGGTGA
CCTCATGCACAGGCTGGGCCACACTGCTCCTCGCGCTGGCTGCTCTGTA
TGTTCCGATAACAAGCACCCGTNTTGAGGAGGAGCTCGGGCCTGGCGGG
CAGAGGCAGGAAAGAGCGGTGGCCAATGGCCTTAGTGAGGAGAAC
GCCACTGTCTGTGCCCC
GAGATGCCCGTCCAGCTGGAGACCTGCCCTCACGACC
GTGGATGCCCTGGCCTGCG
TTCTTCCTGGAGTACCA
GAGCTGGTTGTGGACTTGCTGTACTCGGGCGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGACCAGCCAAGGAGACTAACATT
GCTGTGTTCTGG
GCCTGCTCACAGTGACCTCTCCATCAAGATGTT
CCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCAC
CTTGCCTTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTACGGGCCGTGATTATTAAACGTGGCTT
AATCTGAAGGTTCTCAGTCAAATTCTTGTGATCTACTGATTGTTGGGCATGGCAAGGTTGCTTAAAGGAGC
TTGGCTGGTTGGGCCCTTGTAGCTGACAGAAGGTGGCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGG
CGCTTCTGTTGCTGGCTTGCCCTGGCTCAGTCTGCTAACATACATTGACAATGTTGGCAACTGCACTTCTG
TATTGAGAAGTCTGAAAGGTGCCCTCCACTACGGCCTGACCAAAGAGATAGGAAGAGGGCGCTCACAGATGGCTG
TCCAGACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCCAGAGGTTCTGCAGCTGCCACCATCTCTTAA
TGACAGACGAGCCTGGCTAGACAACCCTGCTACGTGTCCTCGGCAGAGGACGGCAGGCCAGCAATCAGCCC
GTGGACTCTGGCCGGAGCAACCGAAGTAGGGCACGGCCCTTGAGAGATCCACTATTAGAACAGATCATTAA
AAAAATAAAATCGAGCTTGTAGTCTCGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGG
GCAGGGAAAATTCTGAAAACACCACTGCCCTGAAGTCTTCCAAGGTTGTACCCACTGATTCAGATGGTGA
ATTACCAAGCATCAAGATCAATCGAGTAGATCCCAGTAAAGCCTCTCTATTAGGCTGGTGGAGGTAGC
CCCAGGGTCCATATCATTATCCAACACATTATCGTGTGGGTGATGCCAGAGACGGCCGGCTACTGCCAG
GAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGCCCTCACACTACGCTGTGGCTCCTGCC
CAGCCCTGCCAGGTGCTGTGACTGTGATCGTGAACAGAAGTCCCGCAGCAGGAACAATGGACAGGCC
GGATGCCCTACAGACCCCGAGATGACAGCTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGTGGAA
TAAAACCTGGTGCAGGAGTGGATGAGCCTGGGTTTCATCTCAATGTGCTGGATGGCGGTGTCATATCGA
CATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGGCATCAATGGACATGATCTTCGATATGGCAGGCCAGAAAG
TGCCTCATCTGATTCCAGGGCAGTGAAGAGCTGTTACCTCGTGTCCGCCAGGTTCCGCAGCGGAGGCC
CTGACATCTTCAGGAAGCCCGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCAGGGAGAGGAGCAACACT
CCCAAGCCCCCTCCATCTACAATTACTGTGATGAGAAGGTGTTAAATATCCAAAAGACCCGGTGAATCTCT
CGGCATGACCGTCCGAGGGGAGCATCACATAGAGAATGGGATTGCTTATCTATGTCAGTGTGAGCCCG
GAGGAGTCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTGTTGAAATGTTGGATGGGTCGAACGTGACA
GAGGTGAGCCGGAGTGGCAGTGGCATTATTGAAAAGAACATCATCCCTGATAGTACTCAAAGCTTGAAGT
CAAAGAGTATGAGCCCCAGGAAGACTGAGCAGCCAGCAGGCCCTGGACTCCAACACATGGCCCCACCCA
GTGACTGGTCCCCCATCTGGGTCATGTTGCTGGAAATTACACGGTGTGTATAACTGTAAGAGATATTGTATTAA
CGAAGAAACACAGCTGGAAGTCTGGGCTCTGCATTGTAGGAGGTATGAGAAATACAATGGAAACAAACCTTT
TTTCATCAAATCCATTGTTGAGGAACACCGAGCATACAATGATGGAAGAATTAGATGTGGTGTATTCTCTTG
CTGTCATGGTAGAAGTACATCAGGAATGATACATGCTTGGCAAGACTGCTGAAAGAACATTAAAGGAAGA
ATTACTCTAACTATTGTTCTGGCCTGGCACTTTTATTAGAAATCAATGATGGGTAGAGGGAAACAGAAAAAA
TCACAAATAGGCTAAGAAGTGAACACTATATTATCTGTCAGTTTATATTAAAGAAGAACATACATTGT
AAAAATGTCAGGAAAAGTATGATCATCTAACATGAAAGCCAGTACACCTCAGAAAATATGATTCCAAAAAAATTAA
AAACTACTAGTTTTTCTAGTGTGGAGGATTCTCATTACTCTACAAACATTGTTATATTCTTCTATTCAAT
AAAAGCCCTAAACAACTAAATGATGATTTGTATACCCACTGAATTCAAGCTGATTTAAATTAAATTAAATT
GGTATGCTGAAGTCTGCCAAGGGTACATTATGCCATTTTAATTACAGCTAAATATTGTTAAATTAAATT
TTGCTGAGAAACGGTGTGTTCATCAAACAGAAATAAAATTGTTCAAGAGTTAA

1000 800 600 400 200 0

FIGURE 147

MKALLLLVLPWLSPANYIDNVGNLHFPLYSELCKGASHYGLTKDRKRRSQDGCPDGCA
SLTATAPSPEVSAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDGSRNRTRARP
FERSTIRSRSFKKINRALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIP
GEITSIKINRVDPSESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILK
VNGMDISNVPHNYAVRLLRQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFH
VILNKSSPEEQLGIKLVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVLAINGH
DLRYGSPESAAHLIQASERRVHLVVSRQRQRS
PDIFQEAGWNSNGSWSPGPERSNTPKPLHPTITCHEVNQKDPGESLGMTVAGGA
SHREWDLPIYVISVEPGVISRDGRIKTGDILLNVDGVELTEVSSEAVALLKRT
SSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPPSDWSPSWMWLELPRCLYN
CKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDGRIRC
GDILLAVNGRSTSGMIHACLRLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTGAAAAAGAGATATCCACATCTCAAGCCCATAAAGGATAGAAGCT
GCACAGGGCAGTTACTTACTCCAGCACCTCCTCTCCCAGGCAAATGGTGCTGACCATCT
TTGGGATACAATCTCATGGATA CGAGGTTTAACATCATCAGCCCCAAGCAACAATGGTGGC
AATGTT CAGGAGACAGTGACAATTGATAATGAAAAAAATACGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTGGACTATAAACATGGCTACATGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTATCCTGAAGATGGACCATCAGAACATCCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCTCTGGAGTCTGATCAAAGACGTGGATTGGTTCTGCTGGTCAC
CCATTGAGAAACTCTGCAAACATATCCCTTGTATAAGGGGAAAGTGGTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGCCTGGCATCTGGGAATTCAATCTG
TGCAGACATTGTTTAGGATTAGCCCTTGTATCTTCAAAGAAATACATCC
TTGGTTTACACTCAAAGTCAAATTAAATTCTTCCAATGCCCAACTAATTGAGATTC
AGTCAGAAAATATAATGCTGTATTATA

FIGURE 149

MKILVAFLVVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNNLQWYIYEKQALDNMFSNKYTWKYNPLE
SLIKDWDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

FIGURE 150

GGCACGAGCCAGGAACTAGGAGGTCTCACTGCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCCTGGAAGTTCCCCAAAG
 GCCGCTGGGTGCTCATAACCTGCTGTGCACCCCAGCCACCACCGCCCATCACCTATTCCCTC
 TGTGGAACCAAGAACATCAAGGTGCCAAGAAGGTGGTAAGAACCCACGAGCCGGCCTCCTT
 CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGCGTCCT
 CCACCTCAGGTGCCCATGTGGACAGTGCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
 CCAGTGTCTGAGCTGCCGGCAACTTCACTCTGCAGGACAGAGGGCAGGCCAGGGTGG
 GATGATCTGCCAGGCGTCCTCGGCAGCCCACCTATCACCAACAGCCTGATCGGAAGGATG
 GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCCTCCTGCCG
 AGCCAGACATCGGACTGGTTCTGGTGCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
 CCTCACAGTGGTGCCCGAGGTGGTGAAGATGGAGGACTGGCAGGGTCCCTGGAGA
 GCCCCATCCTGCCCTGCCGCTCTACAGGAGCACCCGCGTCTGAGTGAAGAGGAGTTGG
 GGGTTCAAGGATAGGAATGGGAGGTCAGAGGACGCAAAGCAGCAGCCATGTAGAATGAACC
 GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCAGTGTGTTGG
 GTTCATGCAAAATGAGTGTGTTAGCTGCCACAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELRANFTLQDRGAGPRVEMICQASSGSPPITNSLIGKDQVHLQQRPCHRQPANFSFLP
SQTSDFWCQAANNANVQHSALTVVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRINGEVGRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTCTGTGCCTCCGCTTGTGCTCCTG
 CTGTCCGGCTGGTCCCAGGGCTGGCGAGCCGACCCTCACTCTCTTGCTATGACATCACCGT
 CATCCCTAAGTTCAGACCTGGACCACGGTGGTGCCTCAAGGCCAGGTGGATGAAAAGA
 CTTTTCTTCACTATGACTGTGGACAACAAGACAGTCACACCTGTCACTGCCCCCTGGGAAGAAA
 CTAAATGTCACAAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGGTGGACATACT
 TACAGAGCAACTGCGTGACATTCACTGGAGAATTACACACCCAAGGAACCCCTCACCTGC
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTGGCAGTCAGT
 TTCGATGGCAGATCTCCTCCTCTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGCATGGACAGCACC
 CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCCTCAGGCACAACCCAACTCAGGCCAC
 AGCCACCAACCCCTCATCCTTGTGCCTCCTCATCATCCTCCCTGCTTCATCCTCCCTGGCA
 TCTGAGGAGAGTCCTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCCTGTGAGCACG
 GTCTTGATCAAACCTGCCCTCTGTCTGGCAGCTGCCACGACCTACGGTGTATGTCCAGT
 GGCCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTCATTCACTGCCTGATTCTT
 TTGCCAACAAATTACAGCAGTTACCTAACATATTATGCAATTCTCTTGGTGCTACC
 TGATGGAATTCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTCTTCTTC
 TCTTTTGTGGAAATCAAGTACTTCTTGATGATGATCTCTTCTTGCAAATGATATT
 GTCAGTAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTCCGTGCTGAAAGAG
 AATTTTAAATTATTAATAAGAAAAATTATATTAAATGATTGTTCTTGTAGTAATTAT
 TGTTCTGTACTGATATTAAATAAGAGTTCTATTCCAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLGSWSRAGRDPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFL
HYDCGNKTVPVSPLGKKLNVTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTCGAAAACCCATCTATACAAACTATATATTTCATTCTGCTGCTAGCTG
CCTTGGGCCTCACAAATTCATTCTGTTCTGACTTCAAGTTATATACCGTGGA**ATGG**GAG
TTGATCCCAACCATAAACATCGTGGAGGGTTAATTGGTGGTAGCCCTACCCAATTCTG
GTGTGGCTTCTTGAGAGGATTCCACCTCAAAATCATGAACCTGGCTGTTGATCAAAA
GAGAATTGGATTCTACTCTAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTTCAGGTGATGGCAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCAAATTGGAGGCCAAC
CCACAGAACAGCATTCTGGCCAGGCTG**TAA**TCAGAATTGTCGTCGTACATGCTAACAGC
ATTGCTTTTCCCCAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCTTACCTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTCAATGAATTAAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTACCAATGAGAGAAAAAAATGCATTCCTGTAT
CATCCTTTCAATAAAACTGTATTCAATTGAAAAAAAAAAAAAA

FIGURE 155

MELIPTITSWRLILVVALTQFWCGFLCRGFHLQNHELWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKGQPTEQHFWARL

FIGURE 156

GTTCCTCTTCCGAGCCAAATCCAGGCATGGTAATTATGAACGTGCCACACC**ATGAAG**
CTCTTGCGAGGTACTGTGCACCACACCTGAATGCCATCCTGCTCCGTTCGCTA
CCTCACGGCGCAAGTGTGGATTCTGTGCAGGCCATCGCTGCCGCTCAGCCGGCCCC
AGAACTGCCCTCCGTTGCTCGCAGTAACCAGTCAGCAAGGTGGTGTGCACGCGCCGG
GGCCTCTCCGAGGTCCCCCAGGGTATTCCCTCGAACACCCGTACCTAACCTCATGGAGAA
AACATCCAGATGATCCAGGCCGACACCTCCGCCACCTCCACACCTGGAGGTCTGCAGT
TGGGCAGGAACTCCATCCGGCAGATTGAGGTGGGGCCTTCAACGGCTGGCAGCCTAAC
ACCCCTGGAGCTTGCACAACCTGGCTGACAGTCATCCCTAGGGGCTTGAATACTGTC
CAAGCTGCGGGAGCTGGCTTCGAACAAACCCATCGAAAGCATCCCTCTTACGCCTCA
ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCT
GAGGGAGCTTGAGGGCTGTTAACCTCAAGTATCTGAACCTGGCATGTGAAACATTA
AGACATGCCAATCTCACCCCCCTGGTGGGCTGGAGGAGCTGGAGATGTCAGGGAAACACT
TCCCTGAGATCAGGCCTGGCTCCTCCATGGCTGAGCTCCCTCAAGAAGCTGGGTCTAG
AACTCACAGGTCAAGCCTGATTGAGCGGAATGCTTGACGGCTGGCTCACTGTGGAAC
CAAACCTGGCCCACAATAACCTCTTCTTGCCTTACCCGCTGAGGTAC
TGGTGGAGTTGCATCTACACCACAACCTTGAACGTGATTGTGACATTCTGGCTAGCC
TGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCGCTGTCTGCTCCCAT
GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCCTCCAGTGTCTGCC
TCATCATGGACGCACCTCGAGACCTAACATTCTGAGGGTGGATGGCAGAACCTAAC
CGGACTCCCCATGTCTCCGTGAAGTGGTGTGCCCCAATGGGACAGTGTCTAGCCACGC
CTCCGCCACCAAGGATCTGTGCTCAACGACGCCACCTGAAC
TTTCAGACACTGGGTGTACACATGCATGGTGA
GCCTACCTCAATGTGAGCACGGCTGAGCTAACACCTCAACTACAGCTTCTC
AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAAC
CCACGTCCACTGGTACCGAGGCCATATACCACCTCTACCACGGTGTCT
CGTGTGCCAAGCAGGTGGCAGTACCCCGCAGACAGACACCAG
GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTGTGGCAGTGACTCTGCTAG
CTGCCGCATGGTATTGCTTCTATAAACTCGTAAGCGGAC
ACAGCCGCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCC
AGCAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCC
ATGACCATATTAACACTACAACACCTACAAAC
CTGGGAACTCTGCACCCACAGTCACCACTATCTGAAC
TACCAAGGACAAGGTACAGGAAACTCAAATA**TGA**CT
GCAATAGAATGCACACAAAGACAGCAACTTTGTACAGAGTGGGGAGAGACT
TATGCTTATATTAAGTCATGGCTGGTAAAAAAACAGATTAT
CAAAAGTC
AAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAAASAGPQNCPSCSNSQFSKVVC
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFNDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGLFNLKYLNLCMCNIKDMPNLTPLVGLEELEMMSGNHFPEIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFPLRYLVELHLHHNPWNCDCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMVNVAGNSN
ASAYLNVSTAELNTSNYSFFTTVTVETTEISPEDTRKYKPVPTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDTTDKMQTSLDEVMKTTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEAVVLPTIHINYNTYKPAHGAHWTE
NSLGNSLHPTVTTISEPYIIQTHTKDKVQETQI

FIGURE 158

FIGURE 159

MELGCWTQLGLTFLQLLLSSLPREYTVINEACPGAEWNIMCRECCYEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSGGTLDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKİSDLVRRRVLPMQVQSRETPLH
QLYSAAFSKQKLQSAPTPKKPALPFGDLPMDYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSLHKGAFLVCSGALVNE
RTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDRDEKTIQSLQISAIILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSTSfqESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSdictaetggiaavsfgraspepr
WHLMGLVWSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACAGTAATAAAAAACATGGC
 TTCAACCTGACTTCCACCTTCCTACAAATTCCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTTGGGTGGGCCACCAGTAACTACTTCGTGGTGCCATTCAAGAGAGATTCTAAAG
 CAAAGGAGTTCATGGCTAATTCCATAAGACCCTCATTGGGAAGGGAAAAGTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAACCTGACAACACTGTCCTCTGTGTCCTCACCTCAG
 AGGCCAGAGCAAGCTCATTCAAACCCAGATCTCACTTGGAAGAGGTACAGGCAGAAAATC
 CCAAAGTGTCCAGAGGCCGGTATGCCCTCAGGAATGTAAGCTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTACCCACCAGGCTGAAGGTAAAAGT
 TTAATCGAGCCAACCTTGAATGTGGCTATCTAGAACGCCCTCAAGGAAGAAAATTGGGAC
 TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTAAACCTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTGGGGGTGTTACTGCCCTAACGAGAGCAGTTCAAGGTGAATGGATTCTCT
 AACAACTACTGGGGATGGGGAGGCCAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAATTCCCGCCCTGCCTGAAGTGGTAAATATAACATGGTCTTACACCAAGTGTACAGTCTGG
 ACAAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACAGTCTGG
 AGAACAGATGGGTTGAGTAGTTGTTCTTATAAAATTAGTATCTGTGGAACACAATCCTTATA
 TATCAACATCACAGTGGATTCTGGTTGGTGCATGACCCTGGATCTTGGTGAATGGATTGG
 AAGAACTGATTCTTGGTGTGCAATAATTGGCCTAGAGACTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTATTGTTGAGCTGAATTTCCTTTGTATTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAACAGTTGTAACAAGACAGCTTCTTAGTCATTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTGAGGACTCTGGTTGAAGGAGATTATTAAATTGAAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAATAAGACTGCTGAATGTCTGAGAGAACAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATAACAATACTGTTATTCTGTACAATCATCT
 GTGAAGTGGTGGTGTCAAGGTGAGAAGGCCTCACAAAAGAGGGAGAAAAGGCACGAATCA
 GGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAG
 CAGTAGCTGAGCTGGTGCAGGTGCTGATAGCCTTCAGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCTATTAGTTAAAGAGTTTGAAAGTAATATA
 TTTGTACAAGTAGGATATGAATTAGCAGTTACAAGTTACATATTAACATAATAAAATA
 TGTCTATCAAATACCTCTGTAGAAAATGTGAAAAAGCAAA

FIGURE 161

MGFNLTFHLSYKFRLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQLDYGIYVIHQAEGKKFNRAKLLNVGYLEALKEN
WDCFIFHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRSGYFGVTALSREQFFKVNG
FSNNYWGWGGEDEDDLRRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVR
VWRDGILSSCSYKLVSVHNPLYINITVDFWFGA

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCCGGGTCGCGCAGCGGCCTGTGGCGCCGGAGGAGCGACCGCCAGTTCTC
 GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCAACGCTTCTCCGCTCCGGCCCCGA**ATG**
 GCCCAGGCAGTGTGGTCGCGCCTCGGCCGATCCTCTGGCTGCCTGCCTGCCCTGGC
 CCCGGCAGGGTGGCCGCAGGCCTGTATGAACCAATCTCACACCAGTAGCCCTGCCACCA
 CGGGAGCGGTGGTGACCATCTCGCCAGCCTGGTGGCAAGGACAACGGCAGCCTGGCCCTG
 CCCGCTGACGCCACCTCTACCGCTTCACTGGATCCACACCCGCTGGTGGCTACTGGCAA
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTGGCCACGTGCCGGGAATTCCCGG
 TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGCTTG
 GTCTCCCCATCACAGAGTCTCGTGGGGACCTGTTGTCAACCAAGAACACTCCCTACC
 CTGGCCCAGCTCTATCTACTAACAGACCGTCTGAAAGTCTCCTCCTCCACGACCCGA
 GCAACTTCCCAAGACCGCCTGTTCTACAGCTGGACTTCGGGACGGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTCACCGTGAAGCT
 CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGGCCGGATGCCACAGAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCCGCCTCGCTGAAGCTGCAGGAACCCCTCGAGGCATCCAAGTGTGGGG
 CCCACCCAATTCAAGACCTCCAAAAGATGACCGTGAACCTGAACTTCTGGGAGCCCTCC
 TCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCCTCCGCTGGAGGAAGGGAGTGCCACC
 CTGTGTCCGTGGCCAGCACAGCTACAACCTGACCCACACCTCAGGGACCCCTGGGACTAC
 TGCTTCAGCATCCGGCGAGAATATCATCAGCAAGACACATCAGTACCAAGATCCAGGT
 GTGGCCCTCCAGAATCCAGCCGGCTGTCTTGCTTCCATGTGCTACACTTATCACTGTGA
 TGTTGGCCTTCATCATGTACATGACCCCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG
 AACCCGGAGCCACCCCTCTGGGTCAAGGTGCTGCTGCCAGATGTGCTGTGGCCTTCTGCT
 GGAGACTCCATCTGAGTACCTGGAAATTGTTCTGAGAACCAACCGGCTGCTCCGCCCTCT
 ATAAGTCTGTCAAAACTACACCGTGT**TGA**GACTCCCCCTCCCCACCCATCTCAGTGTAA
 CTGACTGCTGACTTGGAGTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGTTCATT
 TGCCTGGGCTGTGGCCTGGATCATCCATCCATCTGTACAGTTCACTGCCACTGCCACAAGCC
 CCTCCCTCTGTCAACCCCTGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCCACTCGTTACCACCCCTGACCCCTACCTTGAAGAGGCTCGTGCAGGACT
 TTGATGCTTGGGTGTTCCGTGTTGACTCCTAGGTGGGCTGGCTGCCACTGCCATTCT
 CTCATATTGGCACATCTGCTGTCCATTGGGGTTCTCAGTTCTCCCCCAGACAGCCCTAC
 CTGTGCCAGAGAGCTAGAAAGAAGGTATAAAGGTTAAAATCCATAACTAAAGGTTGTAC
 ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACCACACACACA
 CACACACACACAGAAATATAACACATGCGTCACATGGCATTTCAGATGATCAGCTCTGTA
 TCTGGTTAAGTCGGTTGCTGGGATGCACCCCTGCACTAGAGCTGAAAGGAAATTGACCTCA
 AGCAGCCCTGACAGGTTCTGGGCCGGCCCTCCCTTGTGCTTGTCTGCAGTTCTGC
 GCCCTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGCAGGACT
 AATACTGAGTGAATGCAGAGTGCTTATAAATATCACCTATTTCAGTAAACCCATCTGTG
 AAACATTCACTGAGGAAAAGGCCTTGCAGCGGTAGAAGAGGTTGAGTCAAGGCCGGCG
 TGGCTCACGCCTGTAATCCCAGCATTGGGAGGCCAGGGCTGGATCACGAGATCAGGA
 GATCGAGACCACCCCTGGCTAACACGGTGAACACCCGCTCTACTAAAAAAATACAAAAAGTT
 AGCCGGCGTGGTGGTGGTGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG
 GTGCGAACCCGGGAGGCAGCTTGCAGTGAGCCAGATGGGCCACTGCACCTCAGCCTGA
 GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRIILWLACLLPWAPAGVAAGLYELNLTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPWPSYLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDGTQ
MVTEDSVVYYNYSIIGTFTVKLVVAEWEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTQKMTVTLNFLGSPLTVCWRLKPECLPSEECHPVSVASTAYNLHTFRDPGD
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCCQMCQGPFLLETPSEYLEIVRENHGLLPPLYKSVKYTV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCAC TGAGCTCCCAGATCT
GGGCCGCTTGCCTCCTGCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTCCA
CAACAGACGGGACAAC TTGCAGAGCTGCAACCCCAGGACAGAGCTGGAGCCAGGCCAGCTG
GATGCCCATGTTCCAGAGGCAGAGGAGGCGAGACACCCACTTCCCCATCTGCATTTCTGCT
GC GGCTGCTGT CATCGATCAAAGTGTGGATGTGCTGCAAGACG**TAG**AACCTACCTGCCCTG
CCCCCGTCCCCTCCCTTATT TATT CCTGCTGCC CAGAACATAGGTCTT GGAATAAAA
TGGCTGGTTCTTTGTTTCCAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA
AAAAAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA

165/330

FIGURE 165

MALSSQIWAACLLLLLLASLTGSVFPQQTGQLAELQPQDRAGARASWMMPMFQRRRRDTH
FPICIFCCGCCHRSKCGMCCKT

FIGURE 166

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTGTTCTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACC**ATG**TTCCTGTTGCTGCCCTTGATAGCCTGATTGTCAACCTCTGGC
 ATCTCCCTGACTGTCCTCTCACCCCTCCTCGTTCATCATAGTGCCAGCCATTGG
 AGTCTCCTTGGTATCCGCAAACACTACATGAAAAGTCTGTTAAAATCTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAAGAACCAACAGCTTACAAGCCCTACACCAAC
 GGAATCATTGCAAAGGATCCCACCTCACTAGAAGAAGAGATCAAAGAGATTGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTGAGCTCTGACATTCTACTTTGCC
 GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCCTGGAACCTGCTGAGCAGAACCAATTATAACTCCAGTACATCAGCCTCGGCTCAC
 GGTCTGTGGGGTTAGGAGTGCTGATTGGTACTGCTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTCACAGGGATTAGCCTCTGGTGGTGGCACAACGTGGTGGGATACTGCCAAT
 GGGAGGTTAAGGAATTATGAGTAAACATGTTACTTAATGTGTTACCGATCTGCGTGC
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGCACGGGGACTCATGGGTGTGATTGAGAGCCATGGTGAAGGCCTG
 CCCACACGTCTGGTTGAGCGCTCGGAAGTGAAGGATGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCATCCTCATCTTCCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAGGGAAGTGGAAATTGGAGGCCACAGTTACCC
 TGTTGCTATCAAGTATGACCCCTCAATTGGCGATGCCCTCTGGAACAGCAGCAAATACGGGA
 TGTTGACGTACCTGCTGCAATGATGACCAGCTGGGCATTGCTGAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTGCGAATAGGGTGAATCTGC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGATGGGCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAAGCTGTACAGCAAGATGATCGTGGGAACCAC
 AAGGACAGGAGCCGCTC**TGA**GCCTGCCCTCAGCTGGCTGGGCCACCGTGCAGGGTGC
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCCCACTGCTGTGCTTCCAGACTCCAGGG
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTCGCCAGCCGAGCAGGGATCCCTGT
 GCACCCGGCGCAGCCTACCCCTGGTGGTCTAAACGGATGCTGCTGGTGTGCAACCCAGGA
 CGAGATGCCATTGTTCTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCA
 CCTTGACGCTGTGCGGGCTGAGTGGTTGGGAGATGTGCCATTGCTGTGCTAGAGAT
 GGCAGTACAAGAGTCTGTTATGCAAGCCGTGCTGCCAGGGATGTGCTGGGGCGGCCACCCG
 CTCTCCAGGAAAGGCACAGCTGAGGCAGTGTGGCTGCCCTCAACATGCCCTCAGC
 CTTGGAGCTGCAGACATGATAGGAAGGAAACTGTCATCTGCAGGGCTTCAGCAAAATG
 AAGGGTTAGATTTATGCTGCTGATGGGTTACTAAAGGGAGGGAAAGAGGCCAGGTG
 GGCGCTGACTGGGCATGGGAGAACGTGTGTTGACTCCAGGCTAACCTGAACCTCC
 ATGTGATGCGCGCTTGTGAATGTTGCTCGGTTCCCCATCTGTAATATGAGTCGGGG
 GAATGGTGGTGATTCTCACCTCACAGGGCTGTTGAGTAAAGTGCCTGCGGGTGA
 AGGACACATCACGTTCAAGTACAGGCCACAAAACGGGGCACGGCAGGCCTGAG
 CTCAGAGCTGCACTGGCTTGAGTAAATAACTGGCTGGTGA
 TGA

FIGURE 167

MFLLLPFDLSLIVNLLGISLTVLFTLLLVFIIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRSGSSKALDNTPEFELSDIFYFCRKGMETIMDDEVTKRFSAAELESWNLLSRTNYNFQYISLRLTVLWGLGVLIRYCFLPLRIALAFTG
ISLLVVGTTVVGYLPGNRFKEFMSKHVHLMCYRICVRALTATITYHDRENPRNGGICVANH
TSPIDVIIASDGYYAMVGQVHGGIMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMMFKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMMTSWAIVCSVWYLPPMTREADEDAVQFANRVKSAIARQGLVDLLWDGGLKREKVKDTE
KEEQQKLYSKMIVGNHKDRSRS

FIGURE 168

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCCTCACCCGGACCCCTGGCCCTCA
 CGTCCTCCAGGG**ATG**GCGCTGGCGGCTTGATGATGCCCTCGGCAGCCTCGGCCTCCAC
 ACCTGGCAGGCCAGGCTGTTCCCACCATCCTGCCCTGGCCTGGCTCCAGACACCTTGAGA
 CGATACTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
 AAATGGCCCACCATGCCCTGCTGCCGAATCCTGGGAGGCAGCCCAGGAGACCTGGGAGGAC
 AAGCGTCGAGGGCTTACCTGCCCTGGCTCAAAGCCCAGAACATGGAATAGCCATTATGGT
 CTACACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGCGGAG
 GCTCCCAGGAGCTTACATGAGGCACTTCCCTCAAGGCCCTGCATTCTACCTGATCCGG
 GCCCTGCAGCTGCTGCGAGGCAGTGGGGCTGCAGCAGGGACCTGGGAGGTGGTGGTCCG
 AGGTGTGGCAGCCTCGCTTGAAACCCAAGAGGCTGGGGACTCTGTCGCTGGGCCAGT
 TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTGGGAGAAGAGGCGGGCTGT
 GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGCCTCCTCTGCCCTCG
 GAAGACTCTGCTCTGGCCCTGGAGAGTTCCAGCTCAGGGTTGGGCC**TGA**AAGTCCA
 ACATCTGCCACTTAGGAGCCCTGGAACGGTGACCTCATATGACGAAGAGGCACCTCCAG
 CAGCCTTGAGAACCAAGAACATGGTCCGGACCCAGCCCTAGCAGCCTCTCCCAACCAGG
 ATGTTGGCCTGGGAGGCCACAGCAGGGCTGAGGGAACCTGCTATGTGATGGGACTTCCT
 GGGACAAGCAAGGAAAGTACTGAGGCAGCCATTGATTGAACGGTGTGCAATGTGGAGACA
 TGGAGTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAH
ALLRESWEAAQETWEDKRRGLTLPPGFKAQNGIAIMVYTNSSNTLYWELNQAVRTGGGSREL
YMRHFPFKALHFYLIRALQLLRGSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTLLLAPGEFQLSGVGP

FIGURE 170

GTGGCTTCATTCAGTGGCTGACTTCCAGAGAGCAAT**ATG**GCTGGTCCCCAACATGCCTCA
CCCTCATCTATACCTTGCGAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCCCGTTGGTGGGCCGTGACTTCCCCCTGAAGTCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAAACCCCTTGTACCACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACGTAAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGACCAATCTGACATGCTGCATG
GAACATGGGAAGAGGATGTGATTATACCTTGGAAAGGCCCTGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGAGAAAGTGTATGACCTTCATCT
GCGTTGCCAGGAACCTGTCAGCAGAAACTCTCAAGCCCCATCCTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCCCTCATGGCCTCTGTGTCTCTGTTGGTGCCCCT
CCTGCTCAGTCTTTGTACTGGGCTATTCTTGGTTCTGAAGAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTAGGGACATTGTCGGAAACTCTAACATATGCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAACTCTAAAGGAAGA
TCCAGCAAATACGGTTACTCCACTGTGGAAATACGGAAAAGATGGAAAATCCCCACTCAC
TGCTCACGATGCCAGACACACCAAGGCTATTGCCTATGAGAATGTTATC**TAG**ACAGCAGTG
CACTCCCTAACGTCTGCTCA

FIGURE 171

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSKPVMTMGLQSNKNGTCVTNLTCMEHGEEDIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSPIALKLCEGAADDPDSSMVLLCLLVPLLLSLFVLGLFLW
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

FIGURE 172

CTGGTCCCCAACATGCCTCACCCCATCTATATCCTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCGTGAAAGAGCTGGTCGGTCCGGTGGGGCCGTGACTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTCAACACAACCCTCTGTCACCATA
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACGTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTGGCCAGGAACCTGTCAGCAGAAACTTCTCAAGCCCC
ATCCTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCATGGTCCTCCT
GTGTCTCCTGTTGGTCCCCCTCCTGCTCAGTCTTTGTAAGGGCTATTCCTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTGTCGGAA
ACTCCTAACATATGCCCTCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAAATCTAAAGGAAGATCCAGCAAATACGGTTACTCCACTGTGGAAATACCGAAAA
AGATGGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTGCCTATGAG
AATGTTATCTAGACAGCAGTGCACCTCCCTAACGTCAGTCTGCTCAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCTGACAGACAGACAATCCATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTGGACTGACCCCTAGTCTGTGCATGCAGAAGAAGCTAGTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTAGACTTTCTGGAGCAAATCCATGTCTGGAGAA
TTCCTTAGTTCTAAAGTCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGA
AACCTCCAGCTGATGGGCTCTATGGCGAGAACAGATTGAGTTCAGACATCAAGGAAA
GGTTTGACAACTATGTGAGGAGCATGGAATCCTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCCTCAGGCCCGAGAATGAAGAATGCCGTGAGCCTCCAGTGTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCCCTCTATCCATACAGCATCCCCAGTATAAATTCT
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTAAATTCTCTTGATACACCCTGACAAT
TTTCATGAAATTATTCCCTTCCCTGTTCAATAAATGATTACCCTGCACTTAA

FIGURE 174

MKMLLLLCLGLTLVCVHAEEASSTGRNFNVEKINGEWTIILASDKREKIEHGNFRLFLEQ
IHVLENSLVLKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSEDIKERFAQLCEEHGILRENIIDLDSANRCLQARE

FIGURE 175

GGCTCGAGCGTTCTGAGCCAGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTCA~~G~~CCTGCTGGTTACTGCTGTTAGGAGTAGTTCTCAATGCGATA~~C~~CTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTCTAAAACCCATCTCTGCTTGAGTGGTGGTT
CCAGGAATTATAGGAGCAGGTCTGATGCCATTCCAGCAACAACAATGTCCTGACAGCAAG
AAAAAGAGCGTGCTGCAACAA~~C~~AGAACTGGAATGTTCTTCATCATTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTTAAAAGGT CCTCTC
ATGTGTAATTCTCAAGCAACAGTAATGCCATTGTGAATTTCATTGAAAAACATCAGTGA
CATTCCAGAAC~~T~~CCAACTTGCAGTGGTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCCACCAGTAACGACACCAGGCGAGTGGCTGGAGAGCATCTAGTTCCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTCTCAGTATTAGGTCTATTGCT
TGTGGATTCTGGAGGTCTGTTGGCTCAGTCAGATAGTCATCGGTTCTGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTC~~A~~TTGTGTAGTTAATGGAAATAAAATGTAAGTA
TCAGTAGTTGAAAAAAAAAAA

FIGURE 176

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRL
IHFSVFLGLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

FIGURE 177

GTCGAATCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACC**ATG**AGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTGCTGCTACCAGGCCATGCTCTTGTCT
GCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTTGCAGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTAAGAACGACTCTCATTGAAAAAGTCCTGGTGGAAA**TAGT**GAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTCAAAGTCTTCACGACACC
CTGATCTTCACTAAAATTGTAAAGTTAACACGTTGCTTAATAATCACTTGCCCTGC

FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLOQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

FIGURE 179

ATCCGTTCTCTCGCCTGCCAGCTCAGGTGAGCCCTGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGCTGCAGACCCCCGCCCCAGTGCCCTCTCCCCCTGCAGCCCTGCCCTC
GAACTGTGAC**ATG**GAGAGAGTGACCCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTGCCAATAAAGACGATCCCTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTCGGGAGGGCTCCTGCCATTGCTGGGATCGCGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAACGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGC**TGA**GCACAGGACTGCCCTCAGGGATGCCCTGA
AGCCTAACACTGGCCCCCAGCACCTCCTCCCCCTGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTCTGATCAGGAGGTTCTTATGAATTAAACTCG
CCCCACCACCCCCCTCA

FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK
YKSSQKQHQSPVPEKAIPLITPGSATTC

FIGURE 181

GGAGAAGAGGTTGTGGACAAGCTGCTCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCC
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGCCTC
 CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCCTATAACAAC TGCCGCCGGCTCC
 AGTGTTCACAGCCCCAAAACGGAAC TGGTTGGGTACCTGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGGCCACCTATTCCCAGGGCTTACGGT
 ATGGCTGGGTCCCATCATCCCCTCATCGTTTATGCCACCCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTTCATCAGGTTCTGAAGCCCTGG
 CTGGGAGAAGGGACTTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC
 GCCCGCCTTCCATTCAACATCCTGAAGTCCTATATAACGATCTCAACAAGAGTGCAAACA
 TCATGCTGACAAGTGGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTCAGCTTGACAGCCATTG
 TCAGGAGAGGCCAGTGAATATATTGCCACCCTTGAGCTCAGTGCCTTGTAGAGAAAA
 GAAGCCAGCATATCCTCCAGCACATGGACTTCTGTATTACCTCTCCATGACGGCGGCG
 TTCCACAGGGCCTGCCGCCTGGTGCATGACTCACAGACGCTGTCATCCGGAGCGGCGT
 CACCCCTCCCCACTCAGGTATTGATGATTTCAAAGACAAAGCCAAGTCCAAGACTTGG
 ATTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTGGAGGCCATGACACCACGCCAGTGGCCTCTC
 CTGGGTCTGTACAACCTTGCAGGGCACCCAGAATACCAAGGAGCGCTGCCACAGGAGGT
 AAGAGCTCTGAAGGACCGCGATCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCC
 TTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTCATCTCC
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCGAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGAC
 CCCTCCGCTTGACCCAGAGAACAGCAAGGGAGGTACCTCTGGTTTATTCTTCTC
 CGCAGGGCCCAGGAAC TGCATGGCAGGCCTCGCCATGGCGGAGATGAAAGTGGCCTGG
 CGTTGATGCTGCTGCACCTCCGGTCTGCCAGACCAACTGAGCCCCAGGAAGCTGGAA
 TTGATCATGCGGCCGAGGGCGGGCTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCA
GTGACTTCTGACCCATCCACCTGTTTGCAGATTGTCATGAATAAACGGTGCTGTCAA

FIGURE 182

MSLLSLPWGLRPVAMSPWLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWG
HLGLITPTEEGLKDKSTQMSATYSQGFTVWLGPPIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGEGLLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
SRLDLMFEHISLMTLDSLQKCIFSFDHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDAVIREERRTLPTQGIDDFKDKAKSKTLDFIDVLLLSKDEDG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCRQEVAELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCTGC
TGTTTGCTTTCACAGGATTCTTAAATCCTCTTATCTCTTCCTCTGACTCCAGGGA
AATATCCTTCAACTCTCAGCACCTCATGAAGACGCGCCTTAACCTCCGGAGGAGCTAGAAA
GAGCTTCCCTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTAACCCAAGAGGAAATTGAGAAAGTTCAAGGATT
CTCTGGACAAGATCCTAACATTTACTGAGTCATCTTGGCCAGAATCTGGAAACCATA
AGAACACGTGAGACTCCTGATTGCTCTGAAATACTGTGTC**TGA**AGTGAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTGATTGAAAAC
AGTGTGGAGAAAAACTAGGCAAACATCACCCCTGTTCATTTGTTACCTGGAAAATAATCCTCT
ATGTTTGCACAAAAAAAAAAAAAA

FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHE
DARLTPEELERASLLQILPEMLGA
ERGDIIRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRET
PDCFWKYCV

FIGURE 185

GAACATTTAGTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCAC
CCACCTCCGCCAGGAACACTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCC**ATG**CCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCCTGAGCCCTGAACACCAAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAACGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACCTGGAAGTCCGGTTCAACGCCCTTGATGTTGGAATCAAGCTGT
CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGAAGTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCAGCCGACAAG**TGA**TCGCCACAAGCCTACTCACCTCTCT
AAGTTAGAAGCGCTCATCTGGCTTTCGCTTGCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAACGTGA

FIGURE 186

MPSPGTVCSLLLLGMLWLDIAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQOHSQLGKFQDILWEEAKEAPADKO

FIGURE 187

FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLDFLGLVHLGQLLIFHIYLSMSPTLSPRSPQGW
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAEELTPRPAGVVPGA

FIGURE 189

GGAGTGCAGATGGCATCCTCGTTCTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAG
 ATGGAGCTCTCGAAGGCCTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTGGGGCACACAGAAGG
 TGCCCAAGCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTGACATGCCAGTGTCCCTG
 GATGGAGATAACCAACACATCCACCCAGGAGGTGGTACAATAACAACACTGGGAGACTGGGATGA
 CCGGTTCTCCTCCGGAGCTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAG
 AACCAGGGAGAGGTGCCGAAGTTCAATTACACCAGCCAAGAGAGAGGTGAGAAA
 GGACTACTGGAATTGCCACGTTGCAAGGCCATGTCACCCACTCTCCGATTGGAGGGAA
 GCCTGATGGAGAAGGCTCCCTCCCTCCCTGGGCTTGTGGCAAAATCCTA
 TGGTTATCCCTGGAACGCAGATCACCTACATCGACTTCATTCACTCAGCTCCTCTGCT
 ACTAACAGACTTGCTACTCACTGGAACCCCTGCCTGTGGCTCAAACGTAGCGCCTTGCTG
 CTGTTCTCTGTCTGTAGGTCTCCTGGGATGGTGGCCACATGATGTATTACAAGTC
 TTCCAAGCGACTGTCAACTGGTCCAGAAGACTGGAGACCACATGTTGAAATTATGGCTG
 GGCCTTCTACATGGCCTGGCTCTCCTCACCTGCTGCATGGCGTGGCTGTCACCACCTCA
 ACACGTACACCAGGATGGTGGCTCAAGTGCAAGCATAGTAAGAGCTCAAGGAAAAC
 CCGAACTGCCTACCACATCACCACATCAGTGTTCCTCGGCGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTGACCAGCTACCACAGTATAATCAGCCCATCCACTCTGTCTTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAACGAGTTAGGTACATGTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGTTGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTAAGTC
 CTAAGGGATTCTGGGTGCCACTGCTCTTTCTACAGCTCCATCTGTTCACCCAC
 CCCACATCTCACACATCCAGAATTCCCTTTACTGATAGTTCTGTGCCAGGTTCTGGGC
 TAAACCATGGAGATAAAAGAAGAGTAAACACTTCCGACCTAAGGATCTGAAA

0 9 8 7 6 5 4 3 2 1 0

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMSLSSLFSFTSLLSNYWFVGTQKVPKPLCEKGAAKCFDMP
VSLDGDTNTSTQEVVQYNWETGDDRFSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRLETTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCA GCTTGGCCAG **ATGT** GGTTACCCCTGGTCTCCTG
 TCTTTATGTCTTCTCCTCTTCCTATTCTGTCA TCTCCCTCACTTAAGTCTCAGGCCTGTCA
 GCAGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTCAGAGCAAACAGGACAACCTATG
 TTATGGATGTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
 GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
 AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTGCCTGCCATTCCCTCCCAA
 GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
 CAATCTGTGTGGCTAGTGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTGT
 AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCCCTCCCCCTGCCCGCCGTAGATTCA
 GACATTGCCCTGTGTGCCACCAAACCAGGACTTCCCCTGGCTTGCATCCCTGGCTCT
 CTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTCAAGCTCCGTTACT
 ATGGCGATGGCCATGATGTTACAATCCCACCTGCCTGAATAATCAAGTGGAAAGGGAAAGCA
 GAGGGAAATGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCCTGAGGAAAAACCAA
 GGGAAAGCAACAGGAACCTCTGCAACTGGTTTATCGGAAAGATCATCCTGCCTGCAGATGC
 TGTTGAAGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGAAGGAA
 ATAGAACAGTCTGCTGGAGTCAGACCTGGAATTCTGATTCCAACACTCTTATTACCTGCTGG
 AAGTCACTCAGCCTCCCCTAGCCATCTCCAGGGTGACGGAAACCCAGTGTATTACCTGCTGG
 AACCAAGGAAACTAACAAATGTAGGTTACTAGTGAATAACCCAAATGGTTCTCCAATTATGCC
 CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

FIGURE 192

MWPLGLLSLCLSPLPISSPSLKSQACQQLLWTIPLSPLVAFRANRTTYVMDVSTNQGSGME
HRNHLCFCDLYDRATSPPLKCSLL

卷之三

FIGURE 193

GTAGCGCCGCTTGGGTCTCCCGCTGCCGCTGCGCCGCCCTGGAGGCCAGGAGCAGCTACCGCCATGGCAGGCATCAAAGCTTGATTAGTTGCTCTTGAGGAGCAATCGGACTGATGTTTGATGCTTGGATGCCCCCTCCAATATAACAAATACTGGCCCTCTTGTCTATTTCATCCTTCACCTATTCCATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGAAGGAACCTGCCATCTTCCTACAACGGGCATTGCGTCAGCTTGGACTCCCTATTGTATTGCCAGAGCACATCTGATTGAGTGGGAGCTTGTGCACTTGTCTCACAGGAAACACAGTCATCTTGCACACTATACTAGGCTTTCTGGTCTTGGAAAGCAATGACGACTTCAGCTGGCAGCAGTGGTGAAGAAAGAAATTACTGAACATTGTCAATGGACCTTCTGTCATTGTTGCCATTACAGCACACAGGAGATGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTGGGGTATTGTTGGCTCCCTCTCACTTTATTGTAAGCATACTATTTCACAGAGACTTGTGAAGGATTAAAGGATTTCTCTTTGAAAAGCTGACTGATTCACACTTATCTATAGTATGCTTTGTGGTGTCTGCTGAATTAAATATTATGTGTTTCTGTAGTTGATTTTTGAATCAATATGCAATGTTAACACATTTTAATGTAATCATTCGATTGGTAGGAATTCAGAATTCCGGCGCTCTATTACTGGTCAAGTACATCTTCTTAAATTATTAGCCTCATTACAAAAATTATAAAAGTTTCACTGAGGTTGGCATACGTTAGACTGTATACTCAGTGAAATATAGCTGCATTACCTCAGAGCAGACATACAGACGGTTGGCATACGTTAGACTGTATACTCAGTGAAATATAGCTGCATTACCTCAGAGGGCCAAGTGTAAATGCCATGCCCTCGTTAGGGTGTGGTTACTGGTAGACAGATGTTGTGGATTGAAAATTATTGGAATTGCTACAGAGGAGTGCTTCTCAATTGTTAGAAGAATTATGTTAAACCTTAAGGTAAGGGTGTAAAACATTGAGATAAGTTTATTGTTATTGTTAGAGTGAGTTGCAATGTTGGAAGAAATGACATTGAAATTCCAGTTTGAACTCTGTTCTATTATAAGTGAATTTGTGATCTCTATCACCTTCATGTTTACCCCTGTTAAATGGACATACATGGAACCAACTACTGATGAGGGACAGTGTATGTTGCAATATGCCAGAAAACCTCCTCTGCTTCTCTTGTACTTATTGGTATGTTGATATATTACATAAAATAACTTTCAAATATACTGTTAAACACTTAGAAGTGTACTTACCTGGAAAATAATTGCTATGCCGTACATTGAGCTGCCCTCCCTGCAAGGCCTGCCATGATTAACAAGTAACCTGTTAGTCTTACAGATAATTGCAATTACAGTTAAGGATTTAGACCATGGTAATAGTAGTTCTTATTCTCTAAGGTTATATCATATGTAATTAAAAGTATTTTAAGACAAGTCTGTATACCTCTGAACCTGTTGATTGAGTTCATCATGATAGATCTGCTGTTCTCTATAAAAGGCAATTGTTGTGAGTTAATGCAAAGTACCCAAGTCAGCTATAGCAGCTTCAAGAACATACCTGACCAAAAAATTCCAGTAACCAGGCATGATCAATTATAGTGGCTGTTACATCTAATAATTATCAGGACTTTTCAAGGAGTGGGTTAAAAAACATTCAAGTTGGCTGACAGTTGTTAAGGATATTGTTGATGTTATTCTAGTATACTACATAAAATTATTCGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTTGTTATGAAAGTTTATTCTCAAGAAAATGGAATAAATTGGGATTGTTGAGCTTCTTACTAAAGATGCCATAAGCCACAGGTTTATTGCCATACTTAAGCCATGACTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCGGCGTGGCTGGACCTCCACTGGAGGCTGAAAGTGGCTGTTGTTATTATAATGTTGAGATTTCAGATTCAAGGAGAAGGTGAGGTACACATGAGTTAGAGAGCTGGTGAGACAGTGGGAACCTTTGTGCTGTGATCTACTGGACTTTTTTGCAAGGAAGTGCATTCTCTGGTCTTCCCTATTTCAGTTCTGGATGTCAGTGCAGTGCAGTGCACTGCTACTGTTTATCCACTTGGCCACACACTTTCTAACAGCTGCGTATTATTCATATACTAATTGCAATTGGCAGCATTGTGCTTTGACCTTGTATACAGTCTGACATAGTGTGCTCTGATTCTAGGCTAGTTACTGAGATATGAAATTCCATAGAATATGCACTGATAACACATTACCAATTCTCTATGAAAGAAAACTTTGATGATGAAACAAATAAGATTAAATATCTATTAAAAAA

FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTTGIVVSAFGLPIVFARAHLIEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

FIGURE 195

CCACACGGCTCCGCCAACGCGTCCGCCAACGCGTCCGCCAACGCGTCCGCCAACGCGTCCGCCAACGCGTCCGCC
 CACGCCTCCGGTGCAAGCTCGGCCAACACTGCCTGGTGGAGGGAAAGGAGCCCAGGCCCTCTGCCGCTCCC
 CGCGCCGCCGTCCGCACCTCCCCAACCGCCGCCGCCGCCGCCGCCGCCCAAAGCAGTGGTGGAGGGCT
 TCTGCAGCTGCCGGGCGGAATGGCAGCTGTTCCGGAGTAAAAGGTGGCAGCTGGTGGAGTGGTGGAGT
 CAATGACGGACATTAACCAGACTGTCAGATCCTGGGAGTGGCAGGCCCCAGTTGGAGTTTTTCCCCCAC
 AACGTACAGTCGCAACTGCAGAGGGAAAGGAAGGGCGAGGAAGGGCGAAGCTCGGGCTCCGGCACGTAGTGG
 GAAACTTGCAGGGTCTAGAAGTCGCTCCCGCTTGCAGGCCCCGGCTGCAGGCCAGGCCAGCAAAGT
 GAGACATTGTCGCCATGCCAGATCCGCCGGAGGACGGGGCTGCCTCGGAAACACAGAGGGGCTTCTCTC
 GCCCTGCATATAATTAGCTGCACACAAAGGGAGCAGCTGAATGGAGGTTGCACTCTCTGGAAAAGGATTCT
 GACCGAGCGCTTCCAATGGACATTCTCAGTCTCTGGAAAGATTCTCGTA**ATGGATTCTCGCTGCTCGGT**
 CTCTGTCTATACTGGCTGAGGGAGGCCCTCGGGGGTGGTCTGTGTCGCTGGGGCCTGCTTCAGATGCT
 GCGCCGCCCGCCAGCGGGCTGCCAGCTGTGCGGGTGGCAGGGGGCGGCTGCTGTCAGGCCGCTCAACC
 TCACCGAGCGCCGCCAACACCTGTCGCCAGTGCCTGCTGCTGCTGCTGCTACAACAGCCTCTGGAGCTGC
 GCCGGCCAGTTACAGGGGTTAATGCACTGAGCTACAGTGGCTCTATCTGGATCACATCACATCTGCTCGTGC
 GGAGCCTTCAAGAACTGCGCCAGTTAAGGAACACTACGCTGAGTTCCAACCAGATACCCAACTGCCAAC
 CCACCTTCCGGCCCATGCCAACCTGCCAGCTGGACCTCTGTCAGTACAACAGCTGCAGGCCGCTCGGCCGCC
 CTCTTCCACGGGCTGCCAGGCTACCCACGCTGTCAGTACAACAGCCTGTCAGTACAACAGCTGTCAGGCC
 CTTCAGGACTGCCAGCCTCAAGTTCTCGACATCGGATACAATCAGCTCAAGAGTCTGGCGCGCAACTCTT
 TCGCCGGCTTGTAAAGCTCACCGAGCTGCACCTCGAGCACACAGACTTGGTCAAGGTGAACCTGCCCACTTC
 CGGCCCTCATCTCCCTGACTCGCTCTGGCTGCCGGAGAACAGGTTGGCATTGTGGTCAGCTCGCTGGACTG
 GTTTGGAAACCTGGAGAAAATGGACTTGTGGGCAACAGAGATCGAGTACATGGAGCCCCATGTGTCAGACG
 TGCCGACACTGAGTCCCTGAGCTTCAACCGCCTACCTACATCGAGGCCGGATCCTCAACTCTTGG
 AAGTCCCTGACAAGCATCACCTGGCCGGAACCTGTGGGATTGCGGGCGCAACGTGTCGCCCCTAGCCTCGT
 GCTCAGCAACTTCCAGGGCGCTACGATGCAACTTGCAGTGCAGGCCAGCCCCGGAGTACGCACAGGGCGAGG
 TCCCTGGACCGCTGTACGCCCTTACCTGTGAGGATGGGCCAGGCCAACAGCGGCCACCTGCTCTGGCC
 GTCACCAACCGCAGTGTACGGGGCCCCCTGCCAGCTCGGCCAACACGCTCGGGACGGCGGGGAGGGGAGC
 CGACGGCACATTGAGCCTGCCACCGTGGCTTCCAGCGGAGCACGCCAGAACGCCGTGCAGATCCACA
 AGGTGGTACGGGACCATGGCCCTCATCTCTCTCATGTGGCTCTGGTCTACGTGTCCTGGAAAG
 TGTTCCTCCAGGCGCCTACGGCAGCTCAGAGCTGCTTGTACGCCAGGGCGAGAACAGAAAACAGAC
 CATGCATCAGATGGCTGCCATGTCTGCCAGGAATACTACGTTGATTACAACCGAACACATTGAGGGAGCCC
 TGGTGATCATCAACGAGTATGGCTCGTGTACCTGCCACAGCAGGCCCGAGGAATGCGAGGTG**TGATTGTC**
 CAGTGGCTCAACCATGCGCTACCAAATACGCTGGGAGCCGGGAGCAGGCCGGGGGAGCAGGCTGGGT
 CTCCCTGCTGTGCTGTGATATGCTCCTTACTGAAACTTAAAGGGGATCTCTCCAGAGACTTGACATTGTTAG
 CTTTATTGTCATTAACAAAGCAGATTAAACACAACAAAAACCCACCCCCAACACCTCAGGACAGTC
 TATCTTAATTTCATATGAGAAACTCTTCCCTTGAAGATCTGTCATATTCAAGAATCTGAGAGTGTAAA
 AAAGGTGGCCATAAGACAGAGAGAATACTGTTGTTTATGCTACTCTCCACCCCTGCCATGATTA
 AACATCATGATGAGAAGATCTTAAGTCATACGCAATTTCATAGAGAACATTGGAAAGAGGAATCTGCAATC
 TGGGAGCTTAAGAGCAATGATGACCATAGAAAAGCTATGTTCTACTTTGTGTTGTTGTTGCTGTTCTGCG
 TTGTTGTTGCTTGTAGGCAAGCAAACGTTGTCACACAAACGGGAATTAGTCACATCATTCATGCCCTGT
 GCCTCTAGCTCGGAGATTGGTGGGGGGAGGTGGGGGGAAACGCCAGGAATAAGGGAAAGTGGTAGTTTAACT
 AAGGTTTGTAAACACTTGAATCTTCTCAAAATTAAATTATTTAAGCTCAAGAAACTTGTCTGACC
 CCTCTAAGCAAAACTACTAACGATTAAAAGAGAATACTTAAAGGTGAGCCTTGTGTTTATTCTC
 CCACAGAGGGTCTAATCTCATATGCTGTGCTATCTGAAAAGAACTTAAGGCCACAAATTACGCTCGCTG
 GGCATTGTCAGGGATTGACCTCCATTGCACTACCTTCCCAGCTGATTAAGGTTCAAGCAGTGGTATTGAGGT
 TTGCAATATTATAGAAAAAAAGCTTCTCAAAATTGACACTCTCACACCCAGCTTACGCCCTAGTA
 GTTTTGTGGTGGACAGAGGAAGCAGGGTAAATGAGACCTGTGCTCTGCTGCTGAGCTCAAGAAAATAGGCAGT
 CCCTGATGCTCAGATCTAGCCTGATATTAAATAGTTGAGACCACCTACCCACAATGAGCCTAACTCTCCAAAG
 ACTACAAAAGTACCATGCAAAAGGAAGGTTATTCAGTAAAGGAATAGTTCTCAACCATTAAAAATAT
 TCTTCTGAACTCATCAAAAGAAGAGGCCAACCTTCTCTGCCTCAAGAAGGGCAGACATTGGTATG
 ATTTAGCATCAACACACATTATGAGTATATGTAAGTAATCAGAGGGGAAATGCCACTTGTATTCTCCA
 AGTTTTCCAAGCAAGTACACACAGATCTGTTGAGGATTAGGGGCCACTTGTGTTCCGGCTTATTAGTCGA
 CTTGTCAGCAAGTTGATGCTAGTCTATGACATGCCAGTAGAACAGGGCATTGATGGATCACATGAGAT
 GGTAGAAGGAACATCATCACACCCCTCTCACAGAGAAAATTATCAAAGAACAGAAAATTATATCTGTTTGG
 AGCAAGAGTGTCTAAATGTTCAAGGGTAGTCAAAATAACATAAAATTCTCCTCTAGATGAGTGGCGATGTG
 GCTGATTGGCTGCCATTGACAGAATGCAAATAAAAGGAATTAGCTAGAATATGACCAATTAAATGTGCTT
 CTGAAATATATTGAGATAGGTTAGAATGTCA

FIGURE 196

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRPMPNLRSVDSL SYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTELHLEHNDLVKVNFAHFPRILISLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQLDSNRLTIEPRILNSWKSLTSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDAYAFHLCEDGAEPTSG
HLLSAVTNRSDLGPPASSATTLAGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQC FVTQRRKQKQTMHQMAAMSAQEYYVDYKPNH
IEGALVIINEYGSCCTCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGGCGAG**ATG**GGCGTCTGGGCCGGTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCAGTCTCAAACACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCGGACCCCGTGCAGCCGGCGCCGTTGAGTTCCCGGGACAAGATGG
TGTCAAGTCCTGGTGCAAGAAGGTACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTCCCGACTCTGACCGCTTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGACGAGGCACCTGGCCTCTCGTGGACGCCGAGCGCGTGCCCTGCCGC
CACGACGACGTCTTCTTCCGCCTAGTGCCTCCTCCCGCGTGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCAGCATCTCGGCTCTGGCCGGACGTTCACGCGCAGCAGGACCTGG
CTGTTTCCTGGCGTCCCGCGGGGCCCTACGCTTCCACGGGCCGGCGCCT**TGA**CGCTG
GGCCCCGAGGACTGCGCGAACCGTCGGCTCGTGCCTGCGAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCT

FIGURE 198

MGVILGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMILLPLDGEVLASGAGFGVSDVGSHLDGAGEPAVFRSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPASPVRVRSISALGRTFTRDEDLAVFLASR
AGRLRFHGPGALSVGPEDCADPSGCVCGNAAQPWICAALLQP

FIGURE 199

200/330

FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCASFWWNKGLALIFCILQSLALTWYSLSFIP
FARDAVKKCFAVCLA

FIGURE 201

TTGAGCGCAGGTGAGCTCTGCCGTTCCGGGGCGTTCCTCCAGTCACCCCTCCGCCGTTACCCGGCGCG
 CCGAGGGAGTCTCCTCCAGACCCCTCCGTTGCTCCAAACTAATACGGACTGAACGGATCGCTGCGAGGGT
 GGGAGAGAAAATTAGGGGAGAAAGGACAGAGAGAGCAACTACCATCCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTGAAA**ATG**ACTTCGAAATTATCTGGTGTCTTCATACTGCTGACTGAGTCTTC
 AACACCTTCTCCAAGCAGCAAAGGTTCTACTAGTTCTTGATGGATTCCGTTGGGATTACT
 TATATAAAGTCCAACGCCCATTTCAATTATGAAATATGGTGTACGTGAAGCAAGTTACTAATGTT
 TTATTACAAAAACCTACCCATTACATTACTGGTAACGGCTCTTGCAGAGAATCATGGGATTGTTGC
 AAATGATATGTTGATCCTATTCGAACAAATCTTCTCCTGGATCACATGAATATTGATTCCAAGTTT
 GGGAGAAGCAGCACCAATATGGATCACAAACCAGAGGGCAGGACATACTAGTGGTGAGCCATGGCCCGGA
 ACAGATGTAAGGAAACATAAGCGCTTCTACTCATTACATGCCCTACAATGAGTCAGTTTCAATTGAAGATAG
 AGTTGCCAAAATTGTTGAATGGTTACGTCAAAGGCCATAAATCTGGTCTCTATTGGGAAGACCCCTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGCCGTCAATTTCAGATATTGACAAGAAGTAA
 GGATATCTCATACAAATGCTGAAAAGGCAAAGTGTGGAACACTCTGAACCTAATCATCACAAAGTGTATGG
 AATGACGCACTGCTGAGGAAAGGTTAATAGAACTTGACAGTACCTGGATAAAGACCAACTATAACCTGATTG
 ATCAATCTCAGTAGCAGCCATCTGGCCAAAAGAAGGTTAATTTGATGAAGTCTATGAAGCCTAACTCACGCT
 CATCCTAATCTTACTGTTACAAAAAGAAGACGTTCCAGAAAGGTGGCATACAAATACAACAGTCGAATTCA
 ACCAATCATAGCAGTGGCTGATGAAGGGTGGCACATTACAGAATAACTGAGTCAGTTCTGTAGGCAACC
 ACGGTTACGATAATCGTTAGCAGATATGCATCCAATTAGCCCAGTGGCCTGCCTTCAGAAAGAATTTC
 TCAAAAGAAGCCATGAACCTCACAGATTGTAACCCACTACTATGCCACCTCTCAATATCACTGCCATGCCACA
 CAATGGATCATCTGAATGTCAGGATCTGCTCAATTCAAGTCAATGCCAAGGGTGGTCCCTTACACAGAGTA
 CTATACTCCTCCCTGGTAGTGTAAACCAGCAGAATATGACCAAGAGGGTCATACCCATTTCATAGGGTC
 TCTCTGGCAGCATTATAGTGTATTGTAATTTCATTAAGCATTAAATTCAACAGTCACAAATACCTGC
 CTTACAAGATATGCATGCTGAAATAGCTCAACCATTATACAAGCC**TAA**TGTTACTTGAAGTGGATTGATA
 TTGAAGTGGAGATTCCATAATTATGTCAGTGTAAAGGTTCAAATTCTGGAAACCCAGTTCCAAACATCTGC
 AGAAACCATTAAGCAGTTACATATTAGGTATACACACACACACACACACACACACACACGGACAAA
 ATACTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGTCCTCATTGTCAGTGAGCATAGGGATAGATAAG
 ATCCTGCTTATTGGACTTGGCGCAGATAATGTATATATTAGCAACTTGCAGTATGAAAGTACCTTATAT
 ATTGCACTTTAAATTCTCCTGATGGTACTTTAATTGAAATGCACTTATGGACAGTTATGTCTTATAAC
 TTGATTGAAAATGACAACCTTTGCACCCATGTCACAGAATACTGTTACGCATTGTCACAAACTGAAGGAAATT
 TCTAATAATCCGAATAATGAACATAGAAATCTATCTCCATAAATTGAGAGAAGAAGAGGTGATAAGTGTG
 AAATTAAATGTGATAACCTTGAACTTGGAGATGTATTCCAAACAGCAGAATGCAACTGTGGGCAT
 TTCTGTCTTATTCTTCCAGAGAACGTTGTTTCAATTATTCCCTCAAAGAGAGTCACAAACTGACAG
 ATTGTTCTAAATATATTGTTCTGTCATAAAATTATTGTGATTTCTGATGAGTCATATTACTGTGATTTC
 TAATAATGAAGACACCATGAATATACTTTCTTCTATAGTCAGCAATGGCCTGAATAGAAGCAACCAGGCA
 CCATCTCAGCAATGTTCTTGTAAATTATTGCTCCTTGAAAATTAAACTATTACATTACATTAA
 AAATCAAATTGGATAAAAAAAAAAAAAAA

FIGURE 202

MTSKFILVSFILAALSLSTTFSQLDQQKVLLVSDGFRWDYLYKVPTPHHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEATPIW
ITNQRAGHTSGAACMWPGTDVKIHKRFPTHMPYNESVSFEDRVAKIVEWFTSKEPINLGLY
WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
LIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPTQSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTGTGATCCCGATTGCTCCCACGGCGGGACCTTGTAACTGCGGGAGGCCAG
 GACAGGCCAACCGTGCAGGGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCCTGCCTGGTCACACAGCAAAGGAGGCAGAGCCAGAACTCACAA
 CCAGATCCAGAGGAAACAGGGAC**ATG**GCCACCTGGACAAAAGGCAGTCACCCGCAGGGCC
 AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACCTCACGGTCGTGGAGACGA
 CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCTGACGTTGCC
 CCTGCCCTGGCCCCGCACCCAGGGCCCCCTGACTTCAGGGCATGTTGAGGAAACTGTT
 CAGCTCCCACAGGTTTCAGGTATCATCATCTGCTTGGTGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCGACAAGAATAACTATGCTGCCATG
 GTATTCCACTACATGAGCATCACCATTTGGTCTTTTATGATGGAGATCATCTTAAATT
 ATTTGTCTTCCGCCTGAGTTCTTACCCACAAGTTGAGATCCTGGATGCCGTGGTGG
 TGGTCTCATTCATCCTGGACATTGTCCTCCTGGTCCAGGAGCACCAGTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTAGAACCGCAACTCTAACGGTAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCAACACCTTGAGTTAGCTGCTCTGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 AACCTGTAAGGAGAAGCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGTCTGGAGTAAATGTGCTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGCTGGTGTACGACAGAGAACCTGACAGTCAGTCACTGCCAGTT
 TCACCTCAGATTACAAATCACACAGAGCATCTGCCTGTTCAATCACAAGAGAACAAACC
 AAAATCTATAAAGATATTCTGAAAATATGACAGAATTGACAAATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYKKWENEAAAAAQQPPPTPV
SGEEGRAAAAPDVAPAPGPAPRAPLDFRGMLRKLFFSHRFQVIIICLVVLDAALLVLAELILDL
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLLSSFTTSLRSWMPVVVVVSFILDI
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLLRLKQMNVQLAAKIQHLEFS
CSEKPLD

FIGURE 205

CGGCTCGAGCTGAGCCGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCAAC**AT**
GCTCTGTCTGTGCCGTACGTGCCGTATCGGGGAAGCCCAGACGAGTTCCAGTACTTTG
 AGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCCATTTCAGTCAGTGTCTCATCCCCCTCC
 CAGGAATTCTCACCTACCGCCAGTGGAAAGCAGAAAATTGTACAAGCTGGAGATAAGGACCT
 TGATGGCAGCTAGACTTGAAGAATTGTCCATTATCTCAAGATCATGAGAAGAAGCTGA
 GGCTGGTGTAAAGATTTGGACAAAAGAATGATGGACGCATTGACGCCAGGAGATCATG
 CAGTCCCTGCCGGACTTGGAGTCAGAGATATCTGAACAGCAGGAGAAAAATTCTCAAGAG
 CATGGATAAAAACGGCACGATGACCATCGACTGGAACCGAGTGGAGAGACTACCACCTCCTCC
 ACCCGTGGAAAACATCCCCGAGATCATCCTACTGGAGCATTCCACGATCTTGATGTG
 GGTGAGAATCTAACGGTCCCAGTGGAGTTACAGTGGAGGAGAGGCAGACGGGATGTGGT
 GAGACACCTGGTGGCAGGAGTGGGGCAGGGCGTATCCAGAACCTGCACGCCCTGG
 ACAGGCTAACGGTGTCTCATGCAGGCCATGCCCTCCGCAGCAACAACTGGGCATCGTTGG
 GGCTTCACTCAGATGATTGAGAAGGGAGGGCCAGGTCACTCTGGCGGGCAATGGCATCAA
 CGTCCTCAAAATTGCCCGAATCAGCCATCAAATTATGGCTATGAGCAGATCAAGCGCC
 TTGTTGGTAGTGACCAGGAGACTCTGAGGATTCACTGGAGAGGCTTGTGGCAGGGCCTTGGCA
 GGGGCCATGCCAGAGCAGCATCTACCCAAATGGAGGTCTGAAGAACCCGGATGGCGCTGCG
 GAAGACAGGCCAGTACTCAGGAATGCTGGACTGCGCCAGGAGGATCTGGCCAGAGAGGGGG
 TGGCCGCCTCTACAAAGGCTATGTCCCCAACATGCTGGGCATCATCCCCATGCCGGCATC
 GACCTTGCACTACGAGACGCTCAAGAAATGCCCTGGCTGCAGCACTATGCAGTGAACAGCGC
 GGACCCCGCGTGTGCTCTGGCCTGTGGCACCATGTCAGTACCTGTGGCCAGCTGG
 CCAGCTACCCCTGGCCCTAGTCAGGACCCGGATGCAGGCGCAAGCCTCTATTGAGGGCGCT
 CCGGAGGTGACCAGTGGCAGCCTCTCAAACATATCTGCGGACCGAGGGGGCCTTCGGGCT
 GTACAGGGGGCTGGCCCCAACATTCTCATGAAGGTCACTCCAGCTGTGAGCATCAGCTACGTGG
 TCTACGAGAACCTGAAGATCACCTGGCGTGCAGTCGG**TGA**CGGGGGAGGGCCGCC
 GCAGTGGACTCGCTGATCCTGGGCCAGCCTGGGTGTGCAGCCATCTCATTCTGTGAATG
 TGCCAACACTAACGCTGTCTCGAGCCAAGCTGTGAAAACCTAACGCAACCGCAGGGAGGGT
 GGGGAGAGCTGGCAGGCCAGGGCTTGTCTGACCCAGCAGACCCCTCTGGTGGTCC
 AGCGAAGACCACAGGCATTCTTAGGGTCCAGGGTCAGCAGGCTCCGGGCTCACATGTGTA
 GGACAGGACATTCTGCAGTGCCTGCCAATAGTGAGCTGGAGCCTGGAGGCCGTTAGT
 TCTTCCATTTCACCCCTGCAGCCAGCTGTTGGCCACGGCCCTGCCCTCTGGTCTGCCGTGC
 ATCTCCCTGTGCCCTTGCTGCCCTGCTGCTGAGGTAAGGTGGAGGAGGGCTACAG
 CCCACATCCCACCCCTCGTCCAATCCCATAATCCATGATGAAAGGTGAGGTACGTGGCCT
 CCCAGGCCCTGACTTCCAAACCTACAGCATTGACGCCAATTGGCTGTGAAGGAAGAGGAAG
 GATCTGGCCTTGTTGACTGGCATCTGAGCCCTGCTGATGGCTGGGCTCTGGGATGCT
 TGGGAGTGCAGGGGGCTGGCTGCCCTGGCTGCACAGAAGGCAAGTGTGGGCTCA
 TGGTGCTCTGAGCTGGCCTGGACCTGTCAAGGATGGGCCACCTCAGAACCAAACACTCACTG
 TCCCCACTGTGGCATGAGGGCAGTGGAGCACCAGTGTGAGGGCGAAGGGCAGAGCGTTTG
 GTGTTCTGGGAGGGAAAGGAAAAGGTGTTGGAGGGCTTAATTATGGACTGTTGGAAAAGGG
 TTTTGTCCAGAAGGACAAGCCGACAAATGAGCAGCTCTGTGCTCCAGAGGAAGACGAGG
 GAGCAGGAGCTGGCTGACTGCTCAGAGTCGTTCTGACGCCCTGGGGGTTCTGTCCAACC
 CCAGCAGGGCGCAGCGGGACCAGCCCCACATTCCACTTGTGCACTGCTGGAACCTATT
 ATTTGTATTTATTGAAACAGAGTTATGTCATACTATTTATAGATTGTTAAATTAA
 GCTTGTCTTTCAAGTTCAACTTATTGTTATTCATATTGTTGTTGATGTTACCTTCCC
 AAGCCGCCAGTGGATGGAGGAGGAGGAGAAGGGGGCTTGGGCCCTGCAAGTGT
 CTGTCAGAGAAATTCTTCTGGACTGGAGGAGGAGAAGGGGGCTTGGGCCAGAAGGCAGCAGCC
 GCTCCTTCTTGGCAGGTTGGGGAGGGCTTGGGCCCTGCAAGTGTGTTGAGGTTG
 CTGGGGCGTGGAGAGAGAGGGAGGAACCTCAATAACCTTGAAGGTGGAATCCAGTTATTG
 CTGCGCTGCGAGGGTTCTTATTCACTCTTCTGAATGTCAGGCAAGTGTGAGGGCT
 CACTGTGAATTGTGGTGGCGGGGCTGGAGGAGAGGGTGGGGGCTGGCTCCGTCC
 CAGCCTCTGCTGCCCTGCTTAACAATGCCGGCAACTGGCAGCTCACGGTTGCACTTCC
 ATTCCACCAGAATGACCTGATGAGGAAATCTCAATAGGATGCAAGATCAATGCAAAAATT
 GTTATATATGAAACATATAACTGGAGTCGTCAGGAAATTAAAGAAATTAAAGAAATTGG
 AAGTTGTCAATTAAAGCAGCCTCTAATAAGTTGTTCAAAGCTGAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILK
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
WRHLVAGGGAGAVSRTCTAPLDRLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
NVLKIAPESAIKFMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNS
ADPGVFVLLACGTMSSCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATA
GCCTCCCTGGGGCAGATCCTCTTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATCATTGGCTTGGTATTCAGGGAGACACTCCATCACAGTCACTACTGTC
 GCCTCAGCTGGGAACATTGGGAGGATGGAATCCTGAGCTGCACCTTGAAACCTGACATCAA
 ACTTTCTGATATCGTGTGATACAATGGCTGAAGGAAGGTGTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGCGGAGCAGGATGAAATGTTAGGCTGGCAGAGCAGTGTGTT
 GCTGATCAAGTGTGATAGTTGGCAATGCCCTTGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATCATCACTTCTAAAGGCAAGGGAAATGCTAACCTTGAGTATA
 AAACTGGAGCCTTCAGCATGCCGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTCCCCCAGCCCACAGTGGCTGGCATCCAAAGTTGACCA
 GGGAGCCAACCTCTCGGAAGTCTCCAATACCAGCTTGAGCTGAACTCTGAGAAATGTGACCA
 TGAAGGTTGTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGATATCAAAGTGACAGAATCGGAGATCAAAAGGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTCTGTGTCTTCTTGCATCAGCT
 GGGCACTCTGCCTCTCAGCCCTTACCTGATGCTAAATAATGTGCCTGGCCACAAAAAG
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTCACCACAGATATGACCTAG
 TTTTATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCA
 AGAAACAAAAAGAAGCCAAAGCAGAAGGCTCCAATATGAACAAGATAATCTATCTCAA
 GACATATTAGAAGTTGGAAAATAATTGATGTGAACTAGACAAGTGTGTTAAGAGTGATAAG
 TAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTGTCTGAATTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCAAACATATCCACATCTTATATTCCA
 CAAATTAAGCTGTAGTATGTACCTAAGACGCTGCTAATTGACTGCCACTCGCAACTCAGG
 GGCGGCTGCATTAGTAATGGGTCAAATGATTCACTTTATGATGCTTCAAAGGTGCCT
 TGGCTTCTCTCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATATTAGCATAA
 ACAGAGCAGTCGGGGACACCGATTTATAAATAAACTGAGCACCTTCTTTAAACAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 208

MASLGQILFWSIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTD
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFPQPTVVWASQVD
QGANFSEVSNTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTESEIKRR
SHLQLLNSKASLCVSSFFAISWALLPLSPYILMLK

FIGURE 209

GAATTTGAGAAGACAGCGCGTTGCCATGGCGCGTCTCTGGGCAGGTGTTGGCTCTGGT
 GCTGGTGGCCGCTCTGTGGGGTGGCACGCAGCGCTGCTGAAGCAGGGCCTCCGCCGGCTGC
 AGCGGGTTCATGAGCCGACCTGGGCCAGCAGTTGCTACAGGAGATGAAGACCCTTCTTG
 AATACTGAGTACCTGATGCCCTTCTCCTCAACCAGTGTGGATCCCTCTATTACCTCAC
 CTTGGCATCGACAGATCTGACCCCTGGCTGTGCCCATCTGTAACTCTGGCTATCATCTCA
 CACTGATTGTTGGGAAGGCCCTGGAGAAGATATTGGTGGAAAACGTAAGTTAGACTACTGC
 GAGTGCAGGGACGCAGCTGTGGATCTGACATACCTGTGTTAGTCCTCCCAGAACCCAT
 CTCCCCAGAGTGGGTGAGGACACGCCCTTCCATCCTGCCCTTCCCTGCAGCTGTTT
 GCTTCCTGTGGCCATCAGAGTCCCTCCAGCAGTCTGGAGAAAGACAGAGGCTGG
 GTTGGGATTGAAGACCAGACCCATCTGAGCCCTCCTCCAGCCCTGTACAGCTCCTACT
 GGCATGGCTGAGCTCAGACCCCTCCTGATTCTGCCTATTATCCAGGAGCAGTTGCTGGCAT
 GGTGCTACCGTGATAGGAATTCACTCTGCATCACAAGCTCAGTGAGTAAGACCCAGGGC
 AACAGTCTACCCCTTGAGTGGGCCAACCCACTCCAGCTCTGCTGCCCTCAGGAAGCCCT
 GGGCCATGAAGTGCTGGCAGTGAGCGGATGGACCTAGCACTCCCTCTGGCCTTAGCTT
 CCTCCTCTTATGGGATAACAGCTACCTCATGGATCACAATAAGAGAACAGAGTGAAAG
 AGTTTGTAACCTCAAGTGCTGTTCAGCTGCGGGATTTAGCACAGGAGACTCTACGCTCA
 CCCTCAGCAACCTTCTGCCCAAGCAGCTCTCCCTGCTAACATCTCAGGCTCCAGGCCA
 GCCACCATTACTGTGGCCTGATCTGGACTATCATGGTGGCAGGTTCCATGGACTGCAGAACT
 CCAGCTGCATGGAAAGGCCAGCTGCAGACTTGAGGCCAGAAATGCAAACGGGAGGCCTCTG
 GGACTCAGTCAGAGCGCTTGGCTGAATGAGGGTGGAACCGAGGGAAAGGTGCGTCGGA
 GTGGCAGATGCAGGAAATGAGCTGTCTATTAGCCTGCCTGCCCAACCCATGAGGTAGGCAG
 AAATCCTCACTGCCAGCCCTTAAACAGGTAGAGAGCTGTGAGCCCCAGCCCCACCTGAC
 TCCAGCACACCTGGCGAGTAGTAGCTGTCAATAATCTATGAAACAGACAAAAAAA
 AAA

FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLLQEMKTLFLNTEYLMFPL
LNQCGSLLYYLTIASTDLTAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS
RHTCVSSFPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTAGGCTCAGCTTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCTGCCAGGCTGCGAAAAGATTCCGAATAAAACT
 TTGCCAGTGGAAAGTACCTAGTGAAACGGCTTAAGATGCCACTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTGGGAGAAGTCAGCTCCAGCACC**ATG**AAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGCAGCTGTAGAACATCTGAGCTGCGTGCAGTGTAA
 TCATGGAAAAATCCTGTCAACAGCATTGCCCTGAATGCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTCATTTGTAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCTCCCTGAAGAACGTGCTGCCAGCAACGCAGACTGCCCTGCTTGTATG
 AATCTAATGGAACCTCCTGTCGTGGAAGCCCTGAAATGCTATGAAGAAGAACAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGAACATGACATTGAGTCTAACAGTCTCGTGTGAAAGGCTGTC
 CAACGTCAGTAACGCCACCTGTCAGTCCCTGTCGGTGAACAGACTCTGGAGGAGTCA
 TCTTCGAAAGTTGAGTGTCAAATGTAACAGCTAACCCCCACGTCTGCACCAACCACT
 TCCCACAACGTGGCTCCAAAGCTCCCTTACCTCTGGCCCTGCCAGCCTCCTCTCG
 GGGACTGCTGCCCT**TGA**GGTCCCTGGGCTGCACTTGCCAGCACCCATTCTGCTTCTCG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCCCTTTCCCTGCTCTGCCCGTTAACTGC
 CCAGTAAGTGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTGTTCTCATTATTA
 AAGCACTGGTTCACTGCCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQ CNSWEKSCVNSIASECPSHANTSCISSASSSLETPVR
LYQNMFC SAENCSEETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE
CPAC YESNGTSCRGKPWKC YEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFECANVNSLTPTSAPTS HNVGSKASLYLLALASLLL RGLLP

FIGURE 213

GGCCTCGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
 GGGCTTGCTCACTGGCCACCCCTCCAACCCCAAGAGCCCAGCCCC**ATG**GTCCCCGCCGCG
 GCGCGCTGCTGTGGTCCTGCTGCTGAATCTGGTCCCCGGCGGCCGGGGCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTACGCTTGGGGCCCCATGACCCGCAG
 CTACCGGAGCACCGCCCGGACTGGTCTTCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTTGGCGCC
 ACGGTGTCCACCGGCTTAGCCGGTGTCCGCCATTAAACGAGGAGGATGGGTCTCAGAAGA
 GGGGTTGTGATTAATGCCGGAAAGGATAGCACCAGCAGAGAGCTTCCCAGTGCAGCTCCA
 ATACAGCGGGAGTTCCAGCAGCAGGTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCCGCTCCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGTCTACCCGAGCCGGTGGCGTCACCCTACCCACAG
 CCATGCCATCTCTGGAGGATCTGCCGTGGTGTGATGCCCTGGGCCCGTGGCACTGCCAC
 TGCAAGTCGGGACCATGAGCCGGAGCCGGCTGGGAAGCTGCACGCCCTTCCGGCGCCT
 TCGAGTTGGGCGCTGAGCCAGCTCCGCACGGAGCACAAGCCTGCACCTATCAACAATGTC
 CCTGCAACCGACTCGGAAGAGTGCCCCCTGGACACAAGTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCACCACTGACGGACCACCACTACCCCTCCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCCTGCCAGCCCTGGCTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTGGAATAGCCTCTTCAGTGTACAGAGATGCAACCAATA
 GACAGAAACCAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTAACCTCT
 CTTGCCCTTCAATCCTAGCACCCACTAGATTTTAGTACAGAAAAACAAAACGGAAAA
 CACAA

FIGURE 214

MVPAAGALLWVLLNLGPRAGAQQLTQTPTEMQRVSLRGFGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAELLAATVSTGFSRSSAINEEDGSSEEGVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPPTAMPSPEDLRLVLMPWGPWHCHCKSGTMSRSRSRGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCPCNRLREECPLDTSLCTDTNCASQSTTSTRTTTFPTIHLRSSPSLPPASPCPALA
FWKRVIRIGLEDIWNSLSSVFTEMQPIDRNQR

FIGURE 215

CCCGGGTCAACCCACCGTCCGGGAGAAAGGATGGCCGGCTGGCGCGGTTGGCTGCTAGCTGGGCA
 GCGGCCTGGCAGCGCTCCAGGGCACCGTGAGCCGGTGTACCGCGACTCGCTACTGCAGTGCAGAGAGCA
 GAACTGCTCTGGGGCGCTCTGAATCACTCCGCTCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCT
 GTCGGGACGACTGTAAGTATGAGTGTATGTGGGTACCGTTGGCTACCTCCAGGAAGGTACAAAGTGCT
 CAGTCCATGGCAAGTGGCCCTCTCCGGTCTGTCTTCAGAGAGCCGCATGGCCGTGGCCTCGTTCT
 CAATGGCCTGGCCAGCCTGGTGTGCTCTGCCACCTCGTGCACGCCCTCCCCATGTACCA
 CCTGTGTGCCCTCGCCTGGGTGTCCCTCAATGCATGGTCTGGTCCACAGTCTCCACACCAGGGACACTGAC
 CTCACAGAGAAAATGGACTACTCTGTGCCTCACTGTACACTCAATCTACCTGTGCTGCCAGGAC
 CGTGGGCTGCAGCACCCAGCTGGTCACTGCCTCCGGCTCTCTGCTCATGCTGACCGTGACGTCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGCAACGTGGCTATTGGCCTGGTCAACGTG
 GTGTGGTGGCTGGCCTGGTGCCTGTGGAACCAAGCGGGCTGCCACGTGCGCAAGTGCCTGGTGGTGGTCTT
 GCTGCTGCAGGGCTGTCCTGCTGAGCTGCTGACTTCCCACCGCTCTCTGGGTCTGGATGCCATGCA
 TCTGGCACATCAGCACCATCCCTGTCACGCTCTCTTCAGCTTCTGAAAGATGACAGCCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTCAAGCTGGACTGAAGACCTTGGAGCGAGTCTGCCCACTGGGATCCTGCC
 GCCCTGCTGGCCTCCCTCTCCCTCAACCCCTGAGATGATTTCTCTTCAACTCTTGAACTTGGACATGA
 AGGATGTGGGCCAGAACATGTGGCCAGCCCCACCCCTGTTGGCCCTCACAGCCTTGGAGTCTGTTAGGG
 AAGGCCTCCCAGCATCTGGGACTCGAGGTGGGAGGACAGCTGCCCTCTACCTCCTGGAGCTGA
 GTGTGTTCTAGCTCACGGGAGGACAGCTGCCCTGTTCTCCACAGCCTCTCCCCACATCCCCAGCTG
 CCTGGCTGGTCTGTGAAAGCCCTGTCTACCTGGGAGACCAGGGACCTAGGGATACAGGGGTCCC
 CTTCTGTTACCAACCCCCCACCTCCAGGACACCACTAGGTGGTGTGGATGCTGTTCTGGCAGCAA
 GTTACGGCGATTCTCCCATGGATCTGAGGGACCAAGCTGCTGGATTGGAAAGGAGTTACCCCTGACC
 GTTGCCTAGCCAGGTCTCAGGAGGCCTACCATACTCCCTTCAGGCCAGGGCTCCAGCAAGCCCAGGCC
 AGGATCCTGTGCTGTGTTGAGAGCCTGCCACCGCTGTGCGGGAGTGTGGGCCAGGCTGAGTGCATAGG
 TGACAGGGCGTGGACATGGCCTGGGTGTGAGCTCAGGCTAGGTGCGCAGTGTGGAGACAGGGTGTG
 CGGGGAAGAGGTGTGGCTCAAAAGTGTGTGTGCAAGGGGGTGGGTGTGTTAGCGTGGTTAGGGAAACGTGT
 TGCCTGCTGGTGGCATGTGAGATGAGTGAUTGCCGGTAATGTGTCCACAGTTGAGAGGTTGGAGCAGGAT
 GAGGAATCTGTACCATCAATAATCACTGTGGAGCGCCAGCTGCCAAGACGCCACCTGGCGGACAGC
 CAGGAGCTCTCATGCCAGGCTGCCGTGTGCATGTTCCCTGCTGGTGCCCTTGGCCCTCTGCAAAC
 CTCACAGGGTCCCCACACAACAGTGCCCTCAGAACAGCAGGCCCTCGGAGGAGAGAAAGGAAATGGGATGGC
 TGGGCTCTCCATCCCTTCTGCCATGGCTGGCCTCCCTCCAAACCTCCATTCC
 GCTGCCAGCCCCCTTGGCATAGCCTGATTGGGAGGAGGAAGGGCGATTGAGGGAGAAGGGAGAAAGCT
 TATGGCTGGTCTGGTTCTCCCTCCAGAGGGCTTACTGTTCCAGGGTGGCCCTGGGCAGGGCAGGGGCC
 ACACATGCCGTGCCCTGGTAAAGGTGACCCCTGCCATTACAGCAGCCCTGGCATGTTCTGCC
 ATAGAAATGGAGGGAGCTCCAGAAAATTTCCATCCAAAGGCAGTCTCCGGTTGAAGCAGACTGGATTG
 CTCTGCCCTGACCCCTGTCCCTTTGAGGGAGGGAGCTATGCTAGGACTCCAACCTCAGGGACTGGGTG
 GCCTGCGCTAGCTTCTTTGATACTGAAAATTTAAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAATCAA
 TTCCAAGCCTAAAAAAAAAAAAAA

FIGURE 216

MAGLAARLVLLAGAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSRFLFFQE PASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAWVSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVWWLAWCLWNQR
RLPHVRKCVVVVLLLQGLSLLLELLDFPPLFWVLDAAWHISTIPVHVLFSSLEDDSLYLL
KESEDKFKLD

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 217

GGCCGCCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCAAGGTCCGTGA
 CTATGGCTCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGCATGCTGCTGGCTG
 CTGATGGCCGCCTGCTCACCTCTGCCTCAGTCATCAGAACCTGAAGGAGTTGCCCTGAC
 CAACCCAGAGAAGAGCAGCACCAAAGAACGGAGAGAAAAGAACCAAAGCCGAGGAGGAGC
 TGGATGCCGAAGTCCCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTCAGCCAGGG
 CAGGCTGCCCTGCAGGATCCCACGTACGGCTGAATCTCAGACTGGGAAAGAGAGGCAA
 ACTCCAATATGAGGACAAGTCCGAAATAATTGAAAGGAAAAGGCTGGATATCAACACCA
 ACACCTACACATCTCAGGATCTCAAGAGTGCAGTGCAACTGGAAAATTCAAGGAGGGGCAGAGATG
 GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCCTTCCGCCATTGA
 GGAACGTAAAGAAAGACTTTGATGAGCTGAATGTTGTCATTGAGACTGACATGCAGATCATGG
 TACGGCTGATCAACAAGTTCAATAGTCCAGCTCCAGTTGGAAGAGAAAGATTGCTGCGCTC
 TTTGATCTTGAATATTATGTCATCAGATGGACAATGCGCAGGACCTGCTTCCCTTGGTGG
 TCTTCAAGTGGTGATCAATGGCTGAACAGCACAGAGCCCCCTCGTAAGGAGTATGCTGCGT
 TTGTCAGGGCGCTGCCTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATGAAGGGGA
 GCCCTGCAGAAGCTGCTGGTCATCCTGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGT
 CCTGTTGCACTGTGCTCCCTGCTGCCACTTCCCTATGCCAGCGGCAGTCCCTGAAGC
 TCGGGGGGCTGCAGGTCTGAGGACCTGGTCAGGAGAACGGCACGGAGGTGCTGCCGTG
 CGCGTGGTCACACTGCTCTACGACCTGGTCACGGAGAACATGTTGCCAGGAGGAGGCTGA
 GCTGACCCAGGAGATGTCCCCAGAGAACGCTGCAGCAGTATGCCAGGTACACCTCCTGCCAG
 GCCTGTGGAACAGGGCTGGTGCAGATCACGGCCACCTCCTGGCGCTGCCGAGCATGAT
 GCCCGTGAGAACGGTGCAGACACTGGCGCTCCTGACCACCTGCCGGACCGCTACCG
 TCAGGACCCCCAGCTGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCGAGGTGCTGGCCA
 GCCTGGAGCTGCAGGATGGTGGAGACAGGAGGCTACTCCAGGAGCTGCTGGCTCTGTCAAC
 AGCTTGCTGAAGGAGCTGAGATGAGGCCCCACACCAGGACTGGACTGGAGTGGATGCCGCTAGTGA
 GGCTGAGGGGTGCCAGCGTGGTGGCTCTCAGGCAGGAGGACATCTGGCAGTGCCTGGCT
 TGGCCATTAAATGGAAACCTGAAGGCCAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 218

MAPQSLPSSRMAPLGMLLGLLAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAEEEL
DAEVLEVFPHTHEWQALQPQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGRLDINTN
TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
RLINKFNSSSSSLEEKIAALFDLEYYVHQMDNAQDLLSFGLQVINGLNSTEPLVKEYAAF
VLGAAFSNSPKVQVEAIEGGALQKLLVILATEQPLTAKKVLFALCSLLRHFPYAQRQFLKL
GGLQVLRTLTVQEKGTEVLAVRVVTLLYDLVTEKMFAEEEALTQEMSPEKLQQYRQVHLLPG
LWEQGWCEITAHLALPEHDAREKVLQTLGVLLTCRDRYRQDPQLGRTLASLQAELYQVLAS
LELQDGEDEGYFQELLGSVNSLLKELR

Important features:

Signal peptide:

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTCCGTAGAGGAAGTGGCGCGGACCTCATTGGGTTCGGTTCCCCCCCCTCCC
 CTTCCCCGGGGTCTGGGGTGACATTGCACCGCGCCCTCGTGGGTGCGTTGCCACCCCA
 CGCGGACTCCCCAGCTGGCGCGCCCTCCCATTGCCTGTCCTGGTCAGGCCCCACCCCC
 TTCCCACCTGACCAGCC**ATG**GGGGCTCGGGTGTTCGGCTGCACTTCGTCGCGTTCGGC
 CGGGCCTCGCGCTTTCTGATCACTGTGGCTGGGACCCGCTCGCGTTATCATCCTGGT
 CGCAGGGCATTTCGGCTGGTCTCCCTGCTCCTGGCCTCTGGTCTGGTCATCTGG
 TCCATGTGACCGACCGGTCAAGATGCCCGCTCCAGTACGGCCTCCTGATTTGGTGTGCTG
 GTCTCTGTCCTTACAGGAGGTGTTCCGCTTGCCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGGTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCGCCAGATGGCCT
 ATGTTCTGGTCTCTCCTCGGTATCATCAGTGGTGTCTCTGTTATCAATATTTGGCT
 GATGCACCTGGGCAGGTGTTGGATCCATGGAGACTCACCCATTACTTCCTGACTTC
 AGCCTTCTGACAGCAGCATTATCCTGCTCCATACCTTTGGGGAGTTGTGTTCTTGATG
 CCTGTGAGAGGGAGACGGTACTGGGCTTGGGCTGGTGGTTGGGAGTCACCTACTGACATCG
 GGACTGACATTCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCATCTATGCAGTCAGTGT
 TTCCATGGGCTCTGGCCTTCATCACAGCTGGAGGGCCCTCGAAGTATTAGCAGCAGCC
 TCTTGTGTAAGGAC**TGA**CTACCTGGACTGATCGCTGACAGATCCCACCTGCCTGTC
 CCCATGACTGAGCCCAGCCCCAGCCGGTCCATTGCCACATTCTCTGTC
 GGTCTACCCACTACCTCCAGGGTTTGCTTGTCTTTGTGACCGTTAGTCTAAGCTT
 TACCAGGAGCAGCCTGGGTCAGCCAGTCAGTGACTGGTGGGTTGAATCTGCACTTACCC
 CACCACCTGGGACCCCTGTTGTCAGGACTCCCCCTGTCAGTGCTCTGCTCTCAC
 CCTGCCAAGACTCACCTCCCTCCCCCTGCAGGCCAGGGCAGGAGGACAGTCGGGTGAT
 GGTGATTCTGCCCTGCGCATCCACCGAGGACTGAGGAACCTAGGGGGACCCCTGGC
 CTGGGGTGCCCTCCTGATGTCCTGCCCTGTATTCTCCATCTCAGTTCTGGACAGTGCAG
 GTTGCCAAGAAAAGGGACCTAGTTAGCCATTGCCCTGGAGATGAAATTAAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTCTC
 AGGCCTGAGGGGAACCATTGGTGTATAAACCTAAACTGCCTTTTTCTTTT
 GAGGTGGGGGGAGGGAGGGTATATTGGAACTCTCTAACCTCCTGGCTATATTTCTC
 TCCTCGAGTTGCTCCTCATGGCTGGCTCATTCGGCCCTTCTCCTGGTCCCAGACCTT
 GGGGAAAGGAAGGAAGTGCATGTTGGAACTGGCATTACTGGAACATAATGGTTAACCT
 CCTTAACCACCGACATCCCTCCTCCCCAAGGTGAAGTGGAGGGTGCTGTTGAGCTGGC
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAGACTACCATGACATCGTAGGGAAGGAGGG
 GAGATTTTTGTAGTTTAATTGGGTGTTGGAGGGGGGGAGGTTCTATAAAACTGT
 ATCATTCTGCTGAGGGTGGAGTGTCCTTAATCAAGGTGATTGTGATTGGACT
 AAAAAAAAGAATTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAA

220/330

FIGURE 220

MGAAVFFGCTFVAFGPAPALFLITVAGDPLRVIILVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFRAFYKLLKADEGLASLSEDGRSPISIRQMAVSGLS
FGIISGVFSVINILADALGPGVVGIHGDSYYFLTAAIIILLHTFWGVVFFDACCERR
YWALGLVVGSLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

FIGURE 221

AAGCTGGTTAAGGAAGCAGAGGAGGGTAGATTCGTTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTCTGGTCTCTCCCTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTGGCTGATGCANTGGGCCAGGTGTGGTGGGATCCATGGAGAC
TCACCCATTANTCCTGANTCAGCCTTNTGACAGCAGCCATTATCCTGCTC

FIGURE 222

GACCGACC GTTCAGATGCCCGGTTCCAGTACGGCTCCTGATTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTGCC TANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTCCATCCGCCAGATGGCCTATGTTN
TGGTNTTCCTTCGGTATCATCAGTGGTGTNTCTGTTATCAATATTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCTATTAAATTCTGAATT CAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTGAGTTGTGTTTGATGCCTGTGA
GAGGAG

FIGURE 223

NGTTGGAGAAGTGGCGCGACNTTCATTGGGTTCGGTTCCCCCTTCCCTTCCCC
GGGTCTGGGTGACATTGCACGGGCCCTCGTGGGTCGCGTGCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTCCCATTGCCTGCCTGGTCAGGCCCCACCCCCCTCCACNTG
ACCAGCCATGGGGCTGCGGTGTTTCGGCTGCACTTCGTCGCGTTCGGCCGGCTTCG
CGCTTTCTTGATCACTGTGGCTGGGACCCGCTCGCGTTATCATTGGTCCATGTGAC
CGACCGGTCAAGATGCCGGCTCCAGTACGGCCTCTGATTTGGTGCTGCTGTCTGTCC
TTCTACAGGAGGTGTTCCGCTTGCCACTACAAGCTGCTTAAGAAGGCAGATGAGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGCCATGTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTCTTCTGTATCAATATTTGGCTGATGCACTTG
GCCAGGTGTGGTGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTCATTGGGTTTCGGTCCCCCTTCCCNTTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCNTCGGGTGCACCCACGCCACTCCC
CAGNTGGCGCCCTCCATTGCCTGTCAGGCCCCACCCCCCTTCCCACCTGA
CCAGCCATGGGGCTCGGGTGTTCGGCTGCACTTCGTCGCGTTCTGGGCCCTTC
GCGCTTTCTTGATCACTGTGGCTGGGACCCGCTCGCGTTATCATCCTGGTGCAGGGC
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGGTCTGGTCATCTGGTCCATGTGA
CCGACCGGTCAAGATGCCGGCTCCAGTACGGCCTCTGATTTGGTGCCTGTC
CTTCTACAGGAGGTGTTCCGCTTGCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCGCCAGATGGCCTATGTTCTG
GTCTCTCCTCGGTATCATCAGTGGTGTCTCTGTTATCAATATTTGGCTGATGCACCT
GGGCCAGGTGTGGTGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCCAGGAGGAGGCAG
TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCCACCCCC
TACCTGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAAGGAGGAGG
TGTCTGTGCGTCTGCACCCACATCTTCTCTGTCCCCTCCTGCCCTGTCTGGAGGCTGCT
AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCTGATGGTGGCCCCT
CCTTGTGGTCCTCTACCTGGGAAATAAGGTGCAGCGGCCATGGCTACAGCAAGACCCC
CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTGCTTCTGGGGTCACAGAGCATGTT
CTCGCCAACAATGATGTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
GGACCTGGGAGCTGGGCCGGGAAGACGCCGGTCGGATGACAGCAGCAGCCGATCATCA
ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTTGTCTAAGGCCAAC
CAGCTCTACTGCCGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGCCGCCACTGCAG
GAAGAAAGTTTCAGAGTCCGTCTGCCACTACTCCCTGTCAACCAGTTATGAATCTGGGC
AGCAGATGTTCCAGGGGTCAAATCCATCCCCACCCCTGGCTACTCCCACCCCTGGCCACTCT
AACGACCTCATGCTCATCAAACAGAACAGAAGAATTGCTCCACTAAAGATGTCAGACCCAT
CAACGTCTCCTCTCATTGTCCTCTGCTGGACAAAGTGCTTGGTGTCTGGCTGGGACAA
CCAAGAGCCCCAAGTGCACTCCTTAAGGTCTCCAGTGCTTGAATATCAGCGTCTAAGT
CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCCGGTGA
CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGCTGTGGTCTGCAATGGCTCCC
TGCAGGGACTCGTGTCTGGGAGATTACCCCTGTGCCGCCAACAGACGGGTGTCTAC
ACGAACCTCTGCAAGTTACCAAGTGGATCCAGGAAACCATCCAGGCCACTCCTGAGTCT
CCCAGGACTCAGCACACCGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTCAG
ACCCTCATTCTCCCAGAGATGTTGAGAATGTTCATCTCTCCAGGCCCTGACCCCCATGTCT
CCTGGACTCAGGGTCTGCTTCCCCACATTGGCTGACCGTGTCTCTAGTTGAACCCCTGG
GAACAATTCCAAAAGTGTCCAGGGCGGGGTTGCGTCTCAATCTCCCTGGGCACTTCAT
CCTCAAGCTCAGGGCCCATCCCTCTGCAGCTGACCCAAATTAGTCCCAGAAATAAA
CTGAGAAGTGGAAAAAA

FIGURE 226

MATARPPWMWVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLTAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIPHGYSHPGHSNDLMLIKLNRRIRPTKDVRPINVSSHCPAGTKCL
VSGWGTTKSPQVHFVPLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSQGDSGGP
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

FIGURE 227

ATGGTCAACGACCGGTGGAAGACCATGGGCCGCGCTGCCAACCTTGAGGACCGGCCGCGA
 CAAGCCGCAGCGGCCGAGCTCGGGCTACGTGCTGTGACCGTGTGCTGGCCCTGGCTGTGC
 TGCTGGCTGTAGCTGTACCGGTGCCGTGCTTCTGAACACGCCACGCCGGGCACG
 GCGCCCCCACCTGTCGTCAACTGGGCTGCCAGGCCAACAGGCCCTGGTCACTGTGGA
 AAGGGCAGACAGCTCGCACCTCAGCATCCTATTGACCCGCGTGCCCGACCTCACCGACA
 GCTTCGACGCCTGGAGAGGCCAGGCCTCGGTGCTGCAGGCCTGACAGAGCACCAGGCC
 CAGCCACGGCTGGGGCAGCAGGAGCAGGAGCTGCTGGACACGCTGCCGACCAAGCTGCC
 CCGGCTGTGGCCCGAGCCTCAGAGCTGCAGACGGAGTGCATGGGCTGCCAGGGCATG
 GCACGCTGGCCAGGGCTCAGGCCCTGCAGACTGAGCAGGCCCTCATCCAGCTTCTC
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTCAACTCCGTCAAGCAGACATCCTGGATGCC
 GCAGAGGGACCGGGGCTGGGCCGGCCCCGCAACAAAGGCCACCTTCAGAGAGGCCCTGCC
 GGGGAACCCGGCCCCGGGGCTGTGCCACTGGCTCCCGCCCCGAGACTGTCTGGACGTCTC
 CTAAGCGGACAGCAGGACATGGCGTCACTCTGTCTTCCCACCCACTACCCGGCCGGCTT
 CCAGGTGTAUTGTGACATGCGCACGGACGGCGGCGTGGACGGTGTTCAGCGCCGGGAGG
 ACGGCTCCGTGAACCTCTCCGGGGCTGGGACGCGTACCGAGACGGCTTGGCAGGCTCAC
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCCCTGACCAACACAGGCTGCCTACGAGCT
 GCACGTGGACCTGGAGGACTTGAGAATGGCACGCCCTATGCCGCTACGGGAGCTCGGCG
 TGGGCTTGTCTCGTGGACCCCTGAGGAAGACGGTACCCGCTCACCGTGGCTGACTATTCC
 GGCACGTGAGGCACTCCCTCTGAAGCAGCAGCGCATGAGGTTACCACCAAGGACCGTGA
 CAGCGACCATTCAGAGAACAACTGTGCCCTCTACCGCGGTGCCTGGTACCGCAACT
 GCCACACGTCCAACCTCAATGGGAGTACCTGCACGCCCTCATGCCGACGGCTCCTATGCCGACGGC
 GTGGAGTGGCTCTCGTGGACGGCTGGCACTACTCAAGTCTGTAGAGATGAAGATCCG
 GCCGGTCCGGAGGACCGCT**TAG**ACTGGTGCACCTTGTCTGGCCCTGCTGGTCCCTGTGC
 CCCATCCCCGACCCCACCTCACTCTTCGTGAATGTTCTCCACCCACCTGTGCCTGGCGGAC
 CCACCTCCAGTAGGGAGGGCCATCCCTGACACGAAGCTCCCTGGCCGGTGAAGT
 CACACATCGCCTCTCGCCGTCCCCACCCCTCCATTGGCAGCTCACTGATCTTGCCTC
 TGCTGATGGGGCTGGCAAACCTGACGACCCAACTCCTGCCCTGCCCACTGTGACTCCGG
 TGCTGTTGCCCTCCCTGGCAGGATGGTGGAGTCTGCCCAAGGCACCCCTGCCCTGCC
 GGCCAAATACCGCATTATGGGACAGAGAGCAGGGGCAGACAGCACCCCTGGAGTCCTC
 CTAGCAGATCGTGGGAATGTCAGGTCTCTGAGGTCAAGGTCTGAGGCCAGTATCCTCCAG
 CCCTCCCAATGCCAACCCCCACCCCGTTCCCTGGTGCCCAAGAGAACCCACCTCTCCCCCAA
 GGGCCTCAGCCTGGCTGTGGCTGGGCTGGGCCCATCCCTACCGGCCCTGAGGTCAAGGATGG
 GAGCTGCTGCCCTTGGGACCCACGCTCCAAGGCTGAGACAGGAGTCCCTGGAGGCCACCCAC
 CCTGTGCCCGGCAGGCCCTGGGTCTGCAGTCTTACCTGCTGTGCCCACTGCTCTCG
 TCTCAAATGAGGCCAACCCATCCCCACCCAGCTCCGGCGCTCTTACCTGGGAGCAGC
 CGGGGCTGCCATCCATTCTCCTGCCCTGGAAGGTTGGTGGGCCCTGCACCGTGGGCT
 GGACTGCGCTAATGGGAGCTCTGGTTCTGGCTGGGCCCTAGGCAGGGCTGGGATGAG
 GCTTGTACAACCCCCACCAATTCCAGGGACTCCAGGGCTCTGAGGCCCTCCAGGAGG
 GCCTTGGGGTGTATGACCCCTCCCTGAGGTGGCTGTCCATGAGGAGGCCAACCCCTGCC
 ATTGACCGTGGCACCTGGACCCAGGCCAGGCCGGCCGGCGAGTGGTCAAGGGACAGGG
 CCACCTCACCGGCCAAATGGGTGCCGGGACTGGGCACCAAGGCCACCTGGACA
 CTTTCTTGTGAATCCTCCCAACACCCAGCACGCTGTGATCCCCACTCCTTGTGACACA
 TGCAGAGGTGAGACCCGCAGGCCAGGACAGCAGGCCAACAGGCCAGGGCTGGAGGCC
 TCCTCAGCTGTGCTCAGCAGCCCTGGACCCGCCGTGGTACGTCAAGGCCAGATGCAGGG
 CGGCTTTCCAAGGCCCTCTGATGGGGCCTCCGAAAGGGCTGGAGTCAGCCTTGGGAGCT
 GCCTAGCAGCCTCTCCTGGCAGGAGGGAGGTGGCTTCTCCCTCCCAACTGAAGTTGTGCTAAA
 AACAAATAATTGACTGGCACCACTGGGGTTGGTGGAGAGGCCGTGTGACCTGGCTCTC
 TGTCCCAGTGCCACCAGGTCACTGCCACATGCGCAG

FIGURE 228

MVNDRWKTMGAAQLEDPRDKPQRPSCGYVLCTVLLALAVLAVAVTGAVLFLNHAHAPGT
APPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQQA
QPRLVGDQEQUELLDTLADQLPRLARASELQTECMGLRKGHGTLGQGLSALQSEQGRQLIQLL
SESEQHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSQQQDDGVYSVFPTHYPAGFQVYCDMRTDGWTVFQRREDSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENGAYARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLLKHSGMRFTTKDRSDHSENNCAFYRGAWWYRNCHTSNLNGQYLRGAHASYADG
VEWSSWTGWQYSLKFSEMkirPVREDR

FIGURE 229

GCAGTCAGAGACTCCCTGCCCTCGCTGGAAAGAACATTAGGAATGCCTTAGTGCCT
 TGCTTCCTGAACTAGCTCACAGTAGCCCGGCCAGGGCAATCCGACCACATTCACTCT
 CACCGCTGTAGGAATCCAG**AATG**CAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTTGCCACAACCTGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGAC
 TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGCTTTGTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTTCAAGTCCAGAATATAAGCTTGAGGAAGTCTGCAGCATGTGGC
 TGAAAAACTCTGCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTGTACAG
 ACAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAGACAGCAAAAGTTGGAG
 GACTGTAATATTCTGCCTTAGTGAAAACCTTACCATGCTGAAGATAAACAAAGAAGA
 CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTCTACTCTTATTGGACAGGGCTT
 TGCGCCCTGACAGTGGCAAGGCCTGGCTGGATGGATGGAACCCCTTCACTCTGAACCT
 TTCCATATTATAATAGATGTCACCAGCCAAGAAGCAGAGACTGTGTGCCATCCTCAATGG
 GATGATCTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGAC**TGA**TTGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAACAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAAATGGTTCTCGT
 TTTCTGTTAGGATCACCAGCATTCTGAGCTGGTTATGCACGTATTAACAGTCACA
 AGAAGTCTTATTACATGCCACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTG
 GCTTAGAGATAACTTAGCTCTTCTCAATGTCTAATATCACCTCCCTGTTTCA
 GTCTCCTTACACTGGTGAATAAGAAACTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGAC
 AGCAAATACACAAGGAATTCTTTGTTTCAGTTCTACTAGTCACCTCCATCC
 CAGTAAAGACCCATCTGCCTTGTCCATGCCGTTCCAACAGGGATGTCACTGATATGAG
 AATCTCAAATCTCAATGCCATTAAAGCATTCTCCTGTGTCATTAGACTCTGATAATTG
 TCTCCCTCCATAGGAATTCTCCAGGAAAGAAATATATCCCCATCTCGTTCATATCAG
 AACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAGACCAGAAAAAGTGAGCCTTCA
 TCTGCACCTGTAATAGTTCAAGTTCTATTCCATTGACCCATATTACCTTCAG
 GTACTGAAGATTAAATAATAATGAAATACTGTGAAAAA

FIGURE 230

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLTLCLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELOSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEKD

FIGURE 231

AATTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTCAACGTGGCGACCAGTGGCCCTGACCCCTG
CTGACTTTGTGCTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTGTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAGAGTTGCAATTNTCAAGTCCAGAATATAAGCTTGAGGAACCTTGAAGGAGGGCAA
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACCTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACACCACTCCCC

FIGURE 232

GCCGAGCGCAAGAACCTGCGCAGCCCCAGAGCAGCTGCTGGAGGGGAATCGAGGCCGGCTC
 CGGGGATTGGCTGGCCGCTGGCTCTGCGTCTGGGGAGGGAGCGGGCCCGCCCGGGGG
 CCCGAGCCCTCCGGATCCGCCCCCTCCCCGGTCCCAGGGCCCTCGGAGACTCCTCTGGCTGCT
 CTGGGGTTGGGGGGGGGGACCCGGTCCGGGCC **ATG**CGGGCATCGCTGCTGCTG
 TCGGTGCTGCGGCCGCAGGGCCGTGGCGTGGGCATCTCCCTGGGCTTCACCTGAGCCT
 GCTCAGCGTCACCTGGGTGGAGGAGCGTGCGGCCAGGGCCACCTGGAGACTCTG
 AGCTGCCGCCGCGGGCAACACCAACCGCGCGCCGACACTCGGTGCGAGCCGGAGCG
 GAGCGCGAGAAGGCCGGGGCGAAGGCCGGGGAGAATTGGGAGCCGGCTTGGCC
 CTACCACCTGCACAGGCCAGGCCAAAAGGCCGTAGGACCGCTACATCAGCA
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCAACGCTGCC
 ACGCTGGCGTGGCGTGAACCGCACGCTGGGACCCGGCTGGAGCGTGTGGTCTGAC
 GGGCGCACGGGCCGCCGGGCCCCACCTGGCATGGCAGTGGTACGCTGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCACCTGCTGGAGCAGCACGGCAGACTTGAC
 TGGTTCTCCTGGTGCCTGACACCACTACACCGAGGCCACGGCTGGCACGCTTAACCTGG
 CCACCTCAGCCTGGCCTCCGCCACCTGTACCTGGGCCGGCCCCAGGACTTCATGGCG
 GAGAGGCCACCCCGGCCGCTACTGCCACGGAGGCTTGGGCTGCTGTCGCGCATGCTG
 CTGCAACAACCTGCGCCCCCACCTGGAAGGCTGCCGCAACGACATCGTCAGTGCACGCCCC
 CGAGTGGCTGGTCGCTGCATTCTCGATGCCACCGGGGTGGGCTGCACTGGTACCGAGG
 GGGTGCACATAGCCATCTGGAGCTGAGCCCTGGGAGCCAGTGCAGGAGGGGACCC
 TTCCGAAGTGCCTGACAGCCCACCTGTGCGTGACCCGTGACATGTACAGCTGCACAA
 AGCTTCGCCAGACTGAACTGGAACGCACGTACCAAGGAGATCCAGGAGTTACAGTGGGAGA
 TCCAGAATACCAGCCATCTGGCGTTGATGGGACCGGGCAGCTGCTGGCCGTGGTATT
 CCAGCACCATCCGCCGGCCTCCGCTTGAGGTGCTGCCTGGACTACTCACGGAGCA
 GCACGCTTCTCGGCCGATGGCTCACCCGCTGCCACTGCGTGGGCTGACCGGGCTG
 ATGTGGCGATGTTCTGGGACAGCTAGAGGAGCTGAACGCCGCTACCAACCGGCTTG
 CGGCTCCAGAAGCAGCAGCTGGTAATGGCTACCGACGCTTGATCCGGCCGGGTATGGA
 ATACACGCTGGACTTGCAGCTGGAGGACTGACCCCCCAGGGAGGCCGGCCCTCACTC
 GCCGAGTGCAGCTCCGGCGCTGAGCCGCTGGAGATCTGCTGTGCCCTATGCACT
 GAGGCCTCACGCTCACTGTGCTGCTCTAGCTGCGCTGAGCGTACGCTGGCCCTGG
 CTTCTGGAGGCCTTGCCACTGCAGCACTGGAGCCTGGTATGCTGCCAGCCCTGACCC
 TGCTGCTACTGTATGAGCCGCCAGGCCAGCGTGGCCATGCAGATGTCTGCACCT
 GTCAAGGCCACGTGGCAGAGCTGGAGCGGGCTTCCCCGGTGCCATGGCTCAG
 TGTGCAGACAGCCGACCCCTACCACTGCGCCTCATGGATCTACTCTCCAAGAACCG
 TGGACACACTGTTCTGCTGGCGGGCCAGACACGGTGCACGCCTGACTTCTGAACCG
 TGCGCATGCATGCCATCTCCGGCTGGCAGGCCTTCTTCCATGCATTCCAAGCCTCCA
 CCCAGGTGGCCCCACCAAGGCCCTGGGCCCCAGAGCTGGCCGTGACACTGGCGCT
 TTGATGCCAGGCAGCCAGCGAGGCCTGCTCTACAACCTCGACTACGTTGCGAGCCGTGG
 CGCCTGGCGGAGCCTCAGAACAGAAGAGGAGCTGCTGGAGAGGCCTGGATGTACGAGCT
 GTTCTCCACTTCTCCAGTCTGCATGTGCTGCCGGCGGTGGAGCCGGCGCTGTCAGCGCT
 ACCGGGCCAGACGTGCAGCGCAGGGCTCAGTGAGGACCTGTACCAACCGCTGCCCTCAGAGC
 GTGCTTGAGGGCTCGGCTCCGAACCCAGCTGGCCATGCCACTGGCCACACCC
 CAACAGCACCT**TGA**ACCCACCCCTGTCCCCGTGGCGATGCCACACCC
 CTCCCCCAAACCAAGAGCCACCTGCCAGCCTCGCTGGCGAGGCTGGCCGTAGCCAGACCC
 AAGCTGGCCCAGTGGTCCCCCTCTGGCTCTGTGGGTCCCTGGCTCTGGACAAAGCACTGG
 GGACGTGCCAGGCCAGGCCACCCACTTCTCATCCAAACCCAGTTCCCTGCCCTGACGCT
 GCTGATTGGCTGTGGCCTCACGTATTATGCACTGAGTACAGTCTGCCTGACGCCAGCC
 CTCTGGGCCCTGGGGCTGGCTGTAGAAGAGTTGGGAGGGAGCTGAGGAGGG
 GCATCTCCAACTTCTCCCTTTGGACCCGCCAGCTGCCCTGCTTAATAAACTGGCCA
 AGTGTGGAAAAA

FIGURE 233

MRASLLSVLRPAGPVAVGISLGFTLSLLSVTWEEPAGPGPPQPGDSELPPRGNTNAARRP
NSVQPGAEEREKPGAGEGAGENWEPRVLVPYHQAQPGQAACKAVRTRYISTELGIRQRLLVAVL
TSQTTLPTLGVAVNRTLGHLERVVFLTGARGRRAPPMAVVTLGEERPIGHLHLALRHLE
QHGDDFDWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQQLRPHLEGCRNDIVSARPDEWLGRCIILDATVGVCCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALTAAHPVRDPVHMYQLHKAFARAELERTYQEIQELQWEIQNTSHLAVGDRA
AAWPVGIPAPSRRPASRFEVLRWDYFTEQHAFSCADGSRPCPLRGADRADVADVLGTALEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLQLEALTPQGGRRPLTRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLYEPRQAQRVA
HADVFAVKAHVAELERRFPGARVPWLSVQTAAPSPLRIMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGPGLPELGRDTGRFDRQAASEACFYN
DYVAARGRLAAASEQEEELLESLDVYELFLHFSSLHVLRAVEPALLQRYRAQTCSARLSEDL
YHRCLQSVLEGLGSRTQLAMLLFEQEQGNST

FIGURE 234

GCTCTGGCCGGCCCCGGGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTGTAT
TGGCAAGCGCTGGCACCTCCCCACACCCCTGCGAACGCTCCCCTAGTGGAGAAAAGGAGT
AGCTATTAGCCAATTGGCAGGGCCCGTTTTAGAAGCTTGATTCTTGAAGATGAAAG
ACTAGCGGAAGCTCTGCCTCTTCCCCAGTGGCGAGGGAACTGGGGGATTGGCTGGAA
CTGTATCCACCAAATGTCACCGATTCTTCTATGCAGGAAATGAGCAGACCCATCAATAA
GAAATTCTCAGCCTGGCGAAAATGGTGGCCCCACGAAGCCACGACAACGGAGGCAAAG
AGGGTTGCTCAACGCCCGCCTATTGAAAACCAAATCAGATCTGGACCTATAGCGTG
GCGGAGGCAGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGATTCT
TTCCCCGCCCTGAGACCCTGCAGCACCATCTGTCAATGGCAGCTGGCTGTTGGTTGAGC
GCTCGCCGTCTTGGCGCAGCGGCACGCGAGGGCTCCGGCCCGTCCGCTGGGA
ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGTGCGGGAAAGCGGCCCCAGAAC
CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAATGTATGAGAAGAACCA
GACTCCCATTGTTATGACAAGGACCCGTTGGACGTCTGGAACATGCGACTTGCTTCTT
CTTGCGTCTCCATCATCCTGGCCTTGGCAGCACCTTGTGGCTATCTGCCTGACTACA
GGATGAAAGAGTGGTCCGCCCGAAGCTGAGAGGTTGTGAAATACCGAGAGGCCAATGGC
CTTCCCACATGGAATCCAATGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAGTG
ACCAGTTGCTAAGTGGGCTCAAGAAGCACCGCCTCCCCACCCCTGCCTGCCATTCTGAC
CTCTTCTCAGAGCACCTAATTAAAGGGCTGAAAGTCTGAA

FIGURE 235

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPS A VAGKRPPEPTTPWQEDPEPE
DENLYEKNPD SHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

FIGURE 236

GGCGGGCTGGGCTGTTGGTTGAGCGCTGCCGTCTTGGCGGAGCGGCACGCGAGGGC
TCCCGGCCGCCCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCGTCCGCT
GTGGCGGGAAAGCGGCCCGAAGACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAACCTGTATGAGAAGAACCCAGACTCCCATGGTTATGACAAGGACCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTGGCGTCCATCATCCTGGTCCTGGCAGCACCC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCGCCGGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTCCATCATGGAATCCAAC TGCTCGACCCAGCA
AGATCCAG

FIGURE 237

GCGGGGGCT**ATG**CCGCTTGCCTGCTCGTCTGGCTCCTGGGGCCCGGCGGCTGGTGCCT
 TGCAGAACCCCCACCGCACAGCCTGCCGGAGGAACTTGTCACTACCCCCGCTGCCTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCCGCACGCCGTGGGATTGGAGCTTCAGCGGGAAAGGAGTG
 TCCCATTACAGGCTCTTCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTACGGGA
 GCTGCACCTGTCATTACACAAGGCTTTGGAGGACCCGATACTGGGGGCCACCCTCCTGC
 AGGCCCATCAGGTGCAGAGCTGTGGTCTGGTCCAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAAAGGAGCTCAGTAATGTCCTCTCAGGGATCTCTGCCTCTCAACTTCATCGA
 CTCCACCAACACAGTCACTCCCACGCTGCCTCCTCAAACCCCTGGGTCTGGCAATGACACTG
 ACCACTACTTCTGCCTATGCTGTGCTGCCGCCGGAGGTGGTCTGCACCGAAAACCTCACC
 CCCTGGAAGAAGCTTGCCTGTAGTCCAAGGCAGGCCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTCCACACCAGCTACCACTCCCAGGCAGTGCATATGCCCTGTTGAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCCTGTCAGTTGTATTGATGCCTTC
 ATCACGGGGCAGGGAAAGAAAGACTGGTCCCTCTCCGGATGTTCTCCGAACCCTCACGGA
 GCCCTGCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACCTACAACCAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTACCTAGGCAC
 CGGAAGACCTATGCCATCTATGACTTGCTGACACCGCCATGATCAACAACCTCTGAAACCT
 CAACATCCAGCTCAAGTGGAAAGAGACCCCCAGAGAATGAGGCCCTCAGTGCCTCTGC
 ATGCCAGCGGTACGTGAGTGGCTATGGCTGCAGAAGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCAGGGCTTCCCGGTGCTGCTGGACACCGTACCTGGTATCTGCG
 GCTGTATGTGCACACCCTACCATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACCAGCCTGCCAGGACCGGCTGCAACCCACCTCCTGGAGATGCTGATTCACTGCC
 GCCAACTCAGTCACCAAGGTTCCATCCAGTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCCTAACCATGGCTTCTATGTCAGCCCATCTGTCTCAGGCCCTGTGCC
 GCATGGTAGCAGCCAAGCCAGTGGACTGGAAAGAGAGTCCCTCTCAACAGCCTGTTCCA
 GTCTCTGATGGCTCTAACTACTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCAGACTTCAGCATGCCCTACACGTGATCTGCCTCACGTGCACTGTGGTGGCGTGT
 GCTACGGCTCTTCTACAATCTCCTACCCGAACCTCCACATCGAGGAGCCCCCACAGGT
 GGCCTGGCCAAGCGGCTGGCAACCTTATCCGGCGCGCCCGAGGTGTCCCCCACTC**TGA**TT
 CTTGCCCTTCCAGCAGCTGCAGCTGCCGTTCTCTGGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTGAACCAAAGTGCCTGGACCCAGGTCAGGGC
 CTACAGCTGTGTTGCTCAGTACAGGAGCCACGAGCCAAATGTGGCATTGAATTGAATTAA
 CTTAGAAATTCTACCTCCTCACCTGAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAA
 AGTGGTCGGTGGCTGCTGTATTGGACAGCACAGAAAAAGATTCCATCACCACAGAAAGGTC
 GGCTGGCAGCACTGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCAGTGTAGTGG
 TGGAGTTACTGTTGTGGAATAAAACGGCTGTTCCGTGGAAAAAAAAAAAAA

FIGURE 238

MPLALLVLLLLGPWGCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDTVTVDKSWK
ELSNVLSGIFCASLNFIIDSTNTVPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNARCTSISWELRQTLSVVFDAFITG
QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNQLKWKRPPEAPPVFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTVPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIQFERALLKWTEYTPDPNHGYVSPSVLSALVPSMVAAKPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVLNLPTPDFSMPYNVICLTCTVVAVCYGSFYNLLRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTGGCCTCATGGTGTCTCGTTGTGACCCGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAGTGTGTGATTCTGTGAAGGAACTGGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCCCTCAGAAATGATGCTGGGTCTTCTACCTCTGGGGTCACTC
TCAC TTGGCACCTGCCCTGAGGGTCTGAGACTTGAATATGGAAGAAGCAATAACCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTCCC AAAAGAGGGAAAGAGTCACAAAAG
TCCAGACCCCAGGGACGGTACTTCCCTCTACCTGGTGCCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCAAAGAGCTGCCTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCAGTGTCAAGAGAGAAACTGGTCCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTGGACTTCCCAGCCTCTAGAACTGTAAGAAATAATAT
TTGCTGTTATAATCCAA

FIGURE 240

MGSSSFLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 241

AAACTCAGCACCTGCCGGAGTGGCTCATTGTTAACGACAAAGGGTGTGCACTTCTGGCCAGG
AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCAAGGACATGCAGAACCTTCC
TCTAGAACCGACCCACCACCAAGGAGGTCTGCCTGGCTGTGGAGATGCAGGCACCTGAGGCCAAGG
CGTCCAGTGGTCCTGCTCTGGCTGTGGCTTCTCTTCTCTTCCGCTTGCCCTCTTTA
TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCT
CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCAC
TGCAGAGGCCAGGCCAGAGAACAAATGCCCTAACACACAAACCAAGGCCAACGCCACACCA
CCGGAGACAGAGGAAGGAGGCCAACCCAGGCACCCGGAGGAGCAGGACAAGGTGCCAAC
ACAGCACAGAGGGCAGCATGGAAGAGCCCAGAAAAAGAGAACATGGTAACACACTGTC
ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
AGGACACAAAGACGACCAAGGAAATGGGGCCAGACCAGGAAGCTGACGGCCTCAGGAGC
GTGTCAGAGAACGACCAAGGCAAAGCGGCAACCACAGCCAAGACGCTCATTCCAAAAGTCA
GCACAGAATGCTGGCTCCCACAGGAGCAGTGTCAACAAGGAGCAGAACAGGAGTGA
CAGCAGTCATCCCACCTAACGGAGAACCTCAGGCCACCCACCCCTGCCCTTCCAG
AGCCCCACGACGAGAACCAAAGACTGAAGGCCAACCTCAAATCTGAGCCTCGTG
GGATTGAGGAAAAATACAGCTCGAAATAGGAGGCCTCAGACGACTGCCCTGACTCTG
TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAAACTCTTCTGCCAACCTCACTCTC
TTCCTGGACTCCAGACACTCAACCAAGAGTGAAGTGGGACCCCTGGAACACTTGCACCA
CTTGGCTCATGGAGCTCAACTACTCCTGGTGCAGAACGGTCGTGACACGCTCCCTCCAG
TGCCCCAGCAGCAGCTGCTCTGGCAGCCTCCCCCTGGAGCCTCCGGTGCATCACCTGT
GCCGTGGTGGGCAACGGGGCATCCTGAACAACTCCCACATGGGCCAGGAGATAGACAGTCA
CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGGATGTGGGACTC
GGACATCCTCTACGGCTTACCGCTTCTCCCTGACCCAGTCACCTCTTATATTGGGCAAT
CGGGGTTCAAGAACGTGCCTCTGGGAAGGACGTCCGCTACTGCACTTCTGGAAAGGCAC
CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTATGTCAAAAACCTT
TCTGGTCAGGCACAGACCCCCAGGAAGCCTTCGGGAAGGCCCTGCACATGGACAGGTACCTG
TTGCTGCACCCAGACTTCTCCGATACATGAAGAACAGGTTCTGAGGTCTAACGACCTGG
TGGTGCCACTGGAGGATAACGCCACACTGGGCCCTCTGCTGCTCACTGCCCTC
AGCTCTGTGACCAGGTGAGTGCCTATGGCTCATCACTGAGGGCCATGAGCCTTCTGAT
CACTACTATGATACATCATGGAGCGGCTGATCTTACATAAACCATGACTCAAGCTGGA
GAGAGAAGTCTGGAAGCGGCTACAGTGAAGGGATAATCGGCTGTACCGCTGGTAC
CCGGAACTGCCAAAGCCAAGAAC**TGA**CCGGGCCAGGGCTGCCATGGTCTCTGCC
CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTGGCCATTCCCATGGCTCAGACTAA
GCTCCAAGCCCTCAGGAGTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCTAAC
GGCAAATGGCTAATTGAGGTCTGAAGTTCTCAGTACATTGCTGTAGGTCTGAGGCCAGG
GATTTTAATTAAATGGGTGATGGTGGCCAATACCACAATTCTGCTGAAAAACACTCTT
CCAGTCCAAAGCTTCTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGATCTG
GTTGAAATTCCAGATCGAGTTACAGTTGAAATCTGAGGTATTACTTAACCTCACTAC
AGATTGTCTAGAAGACCTTCTAGGAGTTATCTGATTCTAGAAGGGCTATAACTGTCTTG
TCTTTAAGCTATTGACAACCTACGTGTTGAGAAAAGTGTAGAAACATGATAATAAC
AAATGATTGTTGTCCATGGAAAGGCCAATAAATTCTACAGTGAaaaaaaaaaaaaaa

FIGURE 242

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
KSQAPTRARRTTIYAEPAPEENNALTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNNGQTRKLTASRTVSEKHQG
KAATTAKTLIPKSQHRLMLAPTGAVSTRTRQKVTTAVIPPKEKKPQATPPPAPFQSPTTQRN
QLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHF
NQSEWDRLEHFAPPFGFMELNYSLVQKVVTFRPPVPQQQQLLASLPAGSLRCITCAVVGNGG
ILNNNSHMQEIDSHDYVFRSGALIKGYEQDVGTRTSFYGFTAFSLTQSLLILGNRGFKNVP
LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFREALHMDRYLLLHPDFL
RYMKNRFLRSKTLGAGHRIYRPTTGALLLLTALLCDQVSAYGFITEGHERFSDHYYDTSW
KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGCACCCCCTCCTGGGGCTGCTGCTGGTGCTGGGCCTCGCCG
GAGCAGCGAGTGGAAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTCTAAAACACCT
TACAGGCCCTTTATTAGTCACAAAGTGCAGCAAACACTTCCATAGACTTATCACAACA
CCAGAGACTGCACCATTCTGCATACTATAAAAGATGCCAGGCTTACCCGGCTGGCT
GTCAGTCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTGGAAACCAACAGGGAAACAGAACTATCTTATACACATCCCCTCATGG
ACAAGAGATTTATTTGCAGACAGACTCTCCATAAGTCCTTGAGTTGTATGTTGTTG
ACAGTTGCAGATATATTCGATAAATCAGTGTACTTGACAGTGTATCTGTCACTTATT

244/330

FIGURE 244

MRGPGHPLLGLLLVLGPSPEQRVEIVPRDLRMKDCKFLKHLTGPLYFSPKCSKHFHRLYHNT
RDCTIPAYYKRCARLLTRIAVSPVCMEDK

FIGURE 245

GGGCTGGGCCCGCCGCAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTCTGGGAGG
 CCCGACCCGGCCGCCAGCCCCACCATGCCACCCGCAGGGCTCCGCCGGCGCGCCG
 CTCACCGCAATCGCTCTGTGGTGCCTGGCTGGCATCCGGGTTAACCTGCGAGTTCTCACCTCT
 GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGTTAACCTGCGAGTTCTCACCTCT
 GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTGCTTATCACCAGAGG
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATGCCCTCAGCTGTGAT
 CCTCTTGTGCTGTGGTGCACCATCTGCTGCTTCCTGTGCTTGTGCTACCTGT
 ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGCAGCCAGTATAACCCATACCCCCAGGACCCAAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCC
 CAGTCTACAACCCCTGCAGCTCCTCCCTATATGCCACCACAGCCCTTTACCCGGGAGCC
TGAGGAAACCAGCCATGTCTGCTGCCCTTCAGTGATGCCAACCTGGGAGATGCCCTCAT
 CCTGTACCTGCATCTGGCCTGGGGTGGCAGGAGTCCTCCAGCCACCAGGCCAGACCAA
 GCCAAGCCCTGGGCCCTACTGGGACAGAGCCCAGGAAAGTGGAACAGGAGCTGAACAG
 ACTATGAGGGTTGGGGAGGGCTTGAATTATGGCTATTTACTGGGGCAAGGGAGG
 GAGATGACAGCCTGGTCACAGTGCCTGTTCAAATAGTCCCTGTGCTCCCAAGATCCCAG
 CCAGGAAGGCTGGGCCCTACTGTTGTCCCTCTGGCTGGGCTGGGGAGGGAGGAGGT
 TCCGTCAGCAGCTGGCAGTAGCCCTCTGGCTGCCACTGGCACATCTGTGCC
 CTAGATTAAGCTGTAAAGACAAAAA

FIGURE 246

MPPAGLRRAAPLTAIALLVLGAPIVLAGEDCLWYLDRNGSWHPGFNCEFFTFC
CRLTLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCF
LCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYP
PSGPAPQYPLYPAGPPVYNPAAPPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCCGGCGGAGTGGTGGCGGGCGCAAGGGTGAGGGCGGGCCAGAA
 CCCCAGGTAGGTAGAGCAAGAAG **ATG** GTTTCTGCCCTCAAATGGTCCCTGCAACCATG
 TCATTCTACTTTCTCACTGTTGGCTCTCTTAACGTGTCCACTCCTCATGGTGTAGAG
 CACTGAAGCATCTCCAAAACGTAGTGTAGGGACACCATTCTGGAAATAAAATACGACTTC
 CTGAGTACGTACATCCCAGTCATTATGATCTCTTGATCCATGCAAACCTTACACGCTGACC
 TTCTGGGAACCACGAAAGTAGAAATCACAGCCAGTCAGCCCACCAGCACCACATCCTGCA
 TAGTCACCACCTGCAGATATCTAGGGCACCTCAGGAAGGGAGCTGGAGAGAGGGCTATCGG
 AAGAACCCCTGCAGGTCTGGAACACCCCCCTCAGGAGCAAATGCACTGCTGGCTCCGAG
 CCCCTCTGTGGGCTCCGTACACAGTTGTCATTCACTATGCTGGCAATCTTCGGAGAC
 TTTCACGGATTACAAAAGCACCTACAGAACAGGAAGGGAAACTGAGGATACTAGCAT
 CAACACAATTGAAACCCACTGCAGCTAGAATGGCCTTCCCTGCTTGATGAACCTGCCTTC
 AAAGCAAGTTCTCAATCAAATTAGAAGAGAGCCAAGGCACCTAGCCATCTCAAATGCC
 ATTGGTGAAATCTGTGACTGTTGCTGAAGGACTCATAGAACACCATTGATGTCAGCAAGATAACC
 AAGAGTGGAGTCAAGGTTCTGTTATGCTGCCCCAGACAAGATAATCAAGCAGATTATGC
 ACTGGATGTCGGTGAECTCTCTAGAATTGAGGATTATTCAGCATAACCGTATCCCC
 TACCCAAACAAGATCTGCTGCTATTCCGACTTCACTGCTGGTCTATGGAAAATGGGAA
 CTGACAACATATAGAGAATCTGCTCTGTTGATGCAGAAAAGTCTTCTGCATCAAGTAA
 GCTTGGCATCACAGTGAETGTTGGCCATGAACCTGGCCACCAGTGGTTGGAACCTGGTCA
 CTATGGAATGGTGAATGATCTTGGCTAAATGAAGGATTGCAAAATTATGGAGTTGTG
 TCTGTCAGTGTGACCCATCCTGAACCTGAAGGTTGGAGATTATTCTTGGCAAAATGGGAGTTGTG
 CGCAATGGAGGTAGATGCTTAAATCCTCACACCCCTGTGCTACACCTGTGGAAAATCCTG
 CTCAGATCCGGAGATGTTGATGATGTTCTTATGATAAGGGAGCTGTTGATATCTGAATATG
 CTAAGGGAGTATCTAGCGTGTGACGCAATTAAAGTGGTATTGACAGTATCTCCAGAAGCA
 TAGCTATAAAACAAAAACGAGGACCTGGGATAGTATGGCAAGTATTGCCCTACAG
 ATGGTGTAAAGGGATGGATGGCTTGCTCTAGAAGTCAACATTCATCTCATCCTCACAT
 TGGCATCAGGAAGGGTGGATGTGAAAACCATGATGAACACTTGGACACTGCAGAGGGTTT
 TCCCCTAATAACCACATCACAGTGAGGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA
 AGGGCTCTGACGGCGCCCCGGACACTGGGTACCTGTGGCATGTTCCATTGACATTCATCACC
 AGCAAATCCAACATGGTCCATCGATTTGCTAAAAACAAAAACAGATGTGTCATCCTCCC
 AGAAGAGGTGGAAATGGATCAAATTAAATGTGGGATGAATGGCTTACATTGTGCAATTACG
 AGGATGATGGATGGACTCTTGACTGGCTTTAAAAGGAACACACAGCAGTCAGCAGT
 AATGATGGGCAAGTCTCATTAACAATGCAATTGCTCAGCTGTCAGCATTGGGAAGCTGTCCAT
 TGAAAAGGCTTGATTTATCCCTGACTTGAAACATGAAACTGAAATTATGCCGTGTTTC
 AAGGTTGAATGAGCTGATCCTATGTATAAGTTAATGGAGAAAAGAGATATGAATGAAGTG
 GAAACTCAATTCAAGGCCTCCTCATCAGGCTGCTAAGGGACCTCATTGATAAGCAGACATG
 GACAGACGGGGCTCAGTCTCAGAGCAAATGCTGGGAGTGAACACTACTCCTCGCCTGTG
 TGCACAACATCAGCCGTGCGTACAGAGGGAGAAGGCTATTCAAGAAAGTGGAGGAATCC
 AATGGAAACTTGAGCCTGCGTGCACGTGACCTTGGCAGTGGTGTGGGGGCCAGAG
 CACAGAAGGCTGGGATTTCTTATAGTAAATATCAGTTTCTTGTCCAGTACTGAGAAAAA
 GCCAAATGAAATTGCCCTCTGCAGAACCCAAAATAAGGAAAGCTTCAATGGCTACTAGAT
 GAAAGCTTAAGGGAGATAAAATAAAAACCTCAGGAGTTTCCACAAATTCTTACACTCATGG
 CAGGAACCCAGTAGGATACCCACTGGCTGGCAATTCTGAGGAAAAGCTGGAACAAACTTG
 TACAAAAGTTGAACCTGGCTCATCTCCATAGCCACATGGTAAATGGGTACAACAAATCAA
 TTCTCCACAAGAACACGGCTGAAGAGGTTAAAGGATTCTCAGCTCTTGAAGAAAACATGG
 TTCTCAGCTCCGTGTGTCACAGACAATTGAAACCATGAGAAAACATGGTGGATGG
 ATAAGAATTGATAAAATCAGAGTGTGGCTGCAAAGTGAAGAAAGCTGAAACGTATG**TAAAAA**
 TTCCTCCCTGCCGGTCTGTTATCTCTAATCACCACATTGTTGAGTGTATTTCAA
 ACTAGAGATGGCTGTTGGCTCCAACGGAGATACTTTTCCCTCAACTCATTGTTGA
 CTATCCCTGTGAAAAGAATAGCTGTTAGTTTCTGATGAATGGCTTTTCAATGAAATGGCTA
 TCGCTACCATGTGTTGTTCATCACAGGTGTTGCCCTGCAACGTAAACCCAAGTGTGG
 TCCCTGCCACAGAAGAATAAGTACCTTATTCTCTAAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
YDLIHNLTTLFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLE
HPPQEIQIALLAPEPLLVLGPYTVVVIHYAGNLSETFHGFYKSTYRTKEGEELRILASTQFEPTA
ARMAFPCFDEPAFKASFISIKIREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA
FIISDFESVSKITSGVKVSVYAVPDKINQADYALDAAVTLLFYEDYFSIPYPLPKQDLAA
IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELHQWFGNLVTMEWWNDL
WLNEGFAKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDMSASICPTDGVKGMGD
FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
TGYLWHVPLTFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
TGLLKGTHTAVSSNDRASLINNAFQLVSIGKLSIEKALDLISLYLKHETEIMPVFQGLNELIP
MYKLMERKRDNEVETQFKAFIIRRDLIDKQTWTDEGSVSEQMLRSELLLLACVHNYQPCV
QRAEGYFRKWKESNGNLSLPVDVTIADVGAQSTEGWDFLYSKYQFSILSSTEKSQIEFALC
RTQNKEKLQWLIDESFKGDKIKTQEFPQILTIGRNPVGYPLAWQFLRKNWNKLVQKFELGS
SSIAHMVMGTTNQFSTRTRLEEVKGFFSSLKENGSQLRCVQQTIETIEENIGWMDKNFDKIR
VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTCA**ATGAGCGCGT**TATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGTGCCAGGA
 CACGTTGATGCTATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGGACTTCTGCAACAACCTCGTTAACCCCTCCGCT
 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGACAACAGAACAGAGATCTGCCCAAGGGGACCACACACTGTTATGAT
 GCCCTCCTCAGGCTCAGGGGAGGGCATCTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAATTGGGCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTCTGACCTGTATGGGACCATCGAATACCGAGATGTGCGAGGTGGGCAGGT
 TTGGCTCAAGAACCCACTGATTGGACCATCGAATACCGAGATGTGCGAGGTGGGCAGGT
 GTGTCAGGAGACGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGACAAAAG
 GCTGCAGCACTGTTGGGCTCAAAATTCCCAGAACGACCAACCATTCACTCAGCCCCCTGG
 GTGCTTGTGGCCTCTACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACCTCCCTCCCTCAAGCTGCCCTGTCCAGGAGACGGCAGTGT
 CTACCTGTGTGCAGCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCAGG
 GGCGCCACTCATTGTTATGATGGGTACATTCTCAGGAGGTGGCTGTCCACCAAAAT
 GAGCATTCAAGGCTGCGTGGCCAACCTCAGCTTGTGAACCACACCAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAACGCGTATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTGGGGGTGGGCTGGCACTGCCAGCGCTGTG
 GTGGGGAGTGGTTGCCCTCCTGCT**TAA**CTCTATTACCCCCACGATTCTCACCGCTGCTGA
 CCACCCACACTCAACCTCCCTGACCTCATAACCTAATGCCCTGGACACCAGATTCTTC
 CCATTCTGTCCATGAATCATCTCCCCACACACAATCATTCTACTCACCTAACAGCA
 AACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCTATGGGAGAGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCCCTGTCTTTCA

FIGURE 250

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPRQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTHCYDGLLRLGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTSNTEMCEVGQVCQETL
LIIDVGLTSTLVGPKGCVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVC

PSC

FIGURE 251

GCGACGGGCAGGACGCCCGTTGCCCTAGCGCGTGCCTCAGGAGTTGGTGTCCTGCCTGCGCT
CAGGATGAGGGGAATCTGGCCCTGGTGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGATGCAGGGAGAGAAGGGAGACAAAGGCGCCCCGGACGCCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAGGAGACATGGGGACAAAGGACAGAAAGGCAGTGTGGGTCGTCA
 GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCCTAATGGAGAACCAAGGCCTCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTCGCC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTAAGGAGGAGAACGCGTACGCGGA
 CGCCCAGCTGTCCCTGCCAGGGCCGGGGCACGCTGAGCATGCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATAACCTGGCGCAAGCCGGCTGGCCCGTGTCTTCATGGCATCAAC
 GACCTGGAGAAGGAGGGCCCTCGTGTACTCTGACCACTCCCCATGCGGACCTCAACAA
 GTGGCGCAGCGGTGAGCCAACAATGCCTACGACGAGGAGACTGCGTGGAGATGGTGGCCT
 CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTGACAAG
 GAGAACATGTGAGCCTCAGGCTGGGCTGCCATTGGGGCCCCACATGTCCTGCAGGGTT
 GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGGAGCTGTCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
 AAAGTGTTCCTGGGTGCTGTCTGAAGAACGAGAGTTCATTACCTGTATTGTAGCCCCA
 ATGTCATTATGTAATTATTACCCAGAATTGCTCTTCCATAAAGCTTGTGCCTTGTCCAAGC
 TATACAATAAAATCTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAA

FIGURE 252

MRGNLALGVVLISLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG
PTGEKGDMGDKQKGSVGRHGKIGPIGSKGEKGDSGDIGPPGPNGEPGLPCECSQLRKAIGE
MDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVMVAS
GGWNDVACHTTMYFMCEFDKENM

FIGURE 253

AGTGACTGCAGCCTTCAGATCCCCTCCACTCGTTCTCTTGCAGGAGCACCGGCAG
CACCAAGTGTGAGGGGGAGCAGGCAGCGGTCTAGCCAGTCCTGATCCTGCCAGACCACC
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACC**ATG**AGGATCATGCTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCCTGGGGGGGGCGCAGCAAGAGGGATCCAGATCTCTACCAAGCTGCTCCAGAGACTCTC
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTCTTGTGGACTTATGGCAAGA
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTCTTACCTTCAGTGAGGGTTCTCGGCC
CTTCATCCAATCAGCTTGGATCCACAGGAAAGTCTCCCTGGAACAGAGGAGCAGAGACC
TTTA**TAA**GA~~C~~TCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTGGCATCCTCAAGT
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCCTGTCCAATCCCCAGGTGCGCACGCTCCTGTTACCCCTTCTTCCCTGTTCTGT
AACATTCTTGTGCTTGACTCCTCTCCATCTTCTACCTGACCCCTGGTGTGGAAACTGCA
TAGTGAATATCCCCAACCCAATGGCATTGACTGTAGAATACCCCTAGAGTTCTGTAGTGT
CCTACATTAAAAATAATGTCTCTCTATTCCCTAACAAATAAGGATTTGCATATGAA
AA

FIGURE 254

MRIMLLFTAILAFSLAQSGAVCKEPQEEVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDMDFFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCTGCTGTGCC
 CGCGCTGTCGCCGCTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTATTG
 GAGCCCTGCAGGAGAGCTCAAGCGCCCAGCTCTGCCAGGAGGCCAGGCTGCCCGTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGCC**ATG**AGCTGCGTCTGGTGGTGTATCCCCCTGGGGC
 TGCTGTTCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCAACGTCACTCTTAGAGGAG
 CTGCTCAGCAAATACCAGCACAAACGAGTCTCACTCCGGTCCGCAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGCAGAGGCTGGCACCGGGGTGGGC
 CTGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCCTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTGTTGTTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAAATGTCATGCCCTG
 AACAC**TAG**ACTCCGGGTTAACCGATCCTGCTTCAGCCTCCAAAGTAGCTGGAACCTACAG
 GCATGCACCATGGTGCCAGCTAGATTTAAATATTTGTGGAGATGGGGGTCTGCTACGT
 TGCCCAGGCTGGTCTTGAACTCCTAGGCTCAAGCAATCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCCGTCTGGCTCTGGCTCTGTTCTTAACATTGCCAAA
 ACAACACACGTGGTTCCCTGTGCAGAGCCTGCCTCGTGCCTCATGTCACTCTGGTAGC
 TCCACTGGGAACACAGCTCAGCCTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
 CTGGGCTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCTGACTTCTC
 CTTAGCCCCTGTGAGCCTCACTTCCACTGGAGAGTCCTCCTCGCTGGTGCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCGGGAAAGGAGCTAACGGTGACAGAACAGCCAAGGTCAACCCCTCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTGGCGATGCTGCTACTGACCCCAAGCTCCAGTG
 TGGAAACTCCTCCTGGCTGGTTCCAGAAGTACAGAGGAATGGACCACAGTCTTCCAGG
 GTCCCTCCTCGTCCACCAACCGGGAGCCTCACCTGGCCATCCGTCAAGCTATGAATGGCTT
 TTTAAACAAACCCACGTCCCAGCCTGGTAACATGGTAAAGCCCCGTCTACAAAAAAATC
 CAAGTTAGCCGGCATGGTGGTGCGCACCTGTAGTCCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGTGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGTGACAGAGCAAGACCCGTCTCAAAA

FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLEEELLSKYQHNESHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSGSGRRGWHRGWLGHQPALFPSQLCSPASACDGWLKVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGG
GTCTGGCTGCCCTTGTCCCTCTTGACCCTCCTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTGCAACTGAAGCTGAAGGAGTCTTCTGACAAATTCCCTCATGAGTCCAGC
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCATCTCCCTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTG
TGTCTTCTGGCCCGGGCTTTGGGCCGGGATGCAGGAGGCAGGCCCGACCCTGTCTT
CAGCAGGCCCCACCCCTGAGTGGCAATAAATAAATTGGTATGCTG

258/330

FIGURE 258

MGSGLPLVLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLHLPSGTS
VTLHHARSQHHVVVCNT

Y. C. S. Y. Y. E. F. D. G. G. D.

FIGURE 259

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAAAGAAGGAAAAACTTCTGAGTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTAAAACAATTAACTGTTAGGATTGCAGT
TATGATTGGATATTATTAATTCTGTTCTGATGTGGGTTCCACTGTGTTCTGTGC
TATTAATATTCACCATTGCAGAAGCCTCATTCACTGTTGAAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTCTCTTAATCAATGCAGAGTTCCCCTCC
CTCCGATTGTTCTAAA**TAA**TTGAAAGATGTCGCTGTGGAAAAAGGCATGTATTAAATCTG
TATGATTCTCAACCATTAGTTGGAAAGGTCTTGAAAGCCAATGAAACTTTTTT
TTTCTTGGCACTAATCAAGTGAGTGTACCTTTCACTTAGTAGGATGTGTTACGCTA
GTAAAATAGAAACCTGTGTTATTCTCAGGTATTTAGAAACAAACAGCCATCATTATT
ATGTGTGTTCTGGCTGTATTCTAAATTATATTTGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTACTTAGATATGCTTCTAGTTGCATTTCTC
AGCCTATGTAAGACTACTTGTGTAATAGCCTTGAAATTACAGTACTGTCTCTACTA
TCTTCAGATTACTGATTCAAATAACCAATTATGTTGTAATTGATATTAATAAACCAGA
ATAAAAGTTCATATCTACCC

260/330

FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

FIGURE 261

GAGGATTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTTGCAGG**ATG**ATGGTGGCCCTT
 CGAGGAGCTCTGCATTGCTGGTTCTGTCAGCTTCTGCCCGCCGAGTGTAC
 CCAGGACCCAGCATGGTGCATTACATCTACCAGCGCTTCGAGTCTGGAGCAAGGGCTGG
 AAAAATGTACCCAAAGCAACGAGGGCATACATTCAAGAATTCCAAGAGTCTCAAAAAAATATA
 TCTGTATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGTAACCTT
 GGCAGTGGAGGTTGAACGTGCCAACAGGGAGATTGACTACATACAATACCTCGAGAGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGATAAAGTC
 TTTGAAAATAGTGAAGAAGATGATGGACACACATGGCTCTGGATGAAAGATGCTGTATA
 ACTCTCAAAGGTGTACTTATTAAATTGGATCCAGAAACACTGTTGGGAATTGCAAAC
 ATACGGGCATTGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCTAACACTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTCTATTTCATAACCAAGCAACCTT
 CTAATGAGATAATCAAATATAACCTGCAGAAGAGGACTGTGGAAGATGCAATGCTGCCA
 GGAGGGTAGGCCGAGCATGGTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGCTCTGGCCATCCACTCTGGCCAGGCACCCATAGCCATTGGTTCTCA
 CAAAGATTGAGCCGGCACACTGGGAGTGGAGCATTGAGGATACCCATGCAAGGCCAG
 GATGCTGAAGCCTCATTCTTGTGTTCTCTATGTGGTCTACAGTACTGGGGCCA
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGACTATCAGTGAGGAGGACTTGC
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGAT
 AAGCAGCTCTATGCCTGGAATGAAGGAAACAGATCATTACAAACTCCAGACAAAGAGAAA
 GCTGCCTCTGAAG**TA**ATGCAATTACAGCTGTGAGAAAGAGCACTGTGGCTTGGCAGCTGTC
 TACAGGACAGTGAGGCTATAGCCCTCACAATATAGTATCCCTCTAATCACACACAGGAAG
 AGTGTGTAGAAGTGGAAATACGTATGCCCTTCCAAATGTCAGTGCTTAGGTATCTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTCAACAATGTCAGCTTCCCTTCA
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTCAAGCCTTGTACT
 GCTCCCAGCATTACTGTAACTCTGCCATCTCCCTCCCACAATTAGAGTGTATGCCAGC
 CCCTAATATTCAACCAGTGCTTCTCTCCCTGGCTTGCTGAAGCTCTCCCTCTTT
 CAAATGTCTATTGATATTCTCCATTTCAGTGCCTCAAGGCTCAGTGTGCTGAGGCTGGCTCA
 CTTTCTTTCTTTTGAGACAAGGCTCAGTGTGCTGAGGCTGGCTGGCTCAACTCC
 AGAGCTCAAGAGATCCTCCTGCCTAGCCTCTAAGTACCTGGATTACAGGCATGTGCCAC
 CACACCTGGCTAAAATACTATTCTTATTGAGGTTAACCTTATTCCTAGCCCTGTC
 CTTCCACTAAGCTGGTAGATGTAATAATAAAAGTGAAGAATATTAACATTGAATATCGCTT
 CCAGGTGTGGAGTGTGACATCATTGAATTCTCGTTCACCTTGTGAAACATGCAACAG
 TCTTACAGCTGTCAATTCTAGAGTTAGGTGAGTAACACAATTACAAAGTGAAGATACAGC
 TAGAAAATACTACAAATCCCAGTCTTCCATTGCCAAGGAAGCATCAAATACGTATGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTCATCGTTCAGCCTAAAATAATAGTCTGTCCC
 TTTAGCCAGTTTCATGTCAGCACAAGACCTTCAATAGGCCTTCAATGATAATTCTCC
 AGAAAACCAGTCTAAGGGTGAGGACCCAACTCTAGCCTCTTGTCTGCTGCTCTGT
 TTCTCTTTCTGCTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAAA

FIGURE 262

MMVALRGASALLVLFLAAFLPPPQCTQDPAMVHYIYQRFRVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQRREIDYIQYLREADECIVSEDKTLAEMLL
QEAEEEKIRTLLNASCDNMLMGIKSLKIVKKMDTHGSWMKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLSWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKIEPGTLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH
YNPRDKQLYAWNENQIIYKLQTKRKLPLK

FIGURE 263

GGGCGCCCGCGTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAAC **ATG**GAGCTCTCGCAGA
 TGTGGAGCTCATGGGGCTGTCGGTGGCTGGCTGGCTGGCCCTGATGGCAGGGCGGC
 GTAGCGGGGGTGGCTGCGCGGGGGAGGAGAGGAGCGGCCGGCCCTGCCAAAAAGC
 AAATGGATTTCACCTGACAAATCTCGGGATCCAAGAACAGAAACAATATCAGCGGATT
 C
 GGAAGGAGAACGCTCAACAAACACAACCTCACCCACCAGCCTCCTGGCTGCAGCTGAAGAGC
 CACAGCAGGGAACATATCTTGATGGACTTAGCAGCAATGGCAAATACCTGGCTACCTGTGC
 AGATGATCGCACCATCCGCATCTGGAGCACCAAGGACTTCCTGCAGCGAGAGCACCGCAGCA
 TGAGAGCCAACGTGGAGCTGGACACGCCACCCCTGGTGCCTCAGCCCTGACTGCAGAGCC
 TTCATCGTCTGGCTGGCCAACGGGGACACCCCTCCGTCTCAAGATGACCAAGCAGGGAGGA
 TGGGGGCTACACCTCACAGCCACCCAGAGGACTTCCTAAAAAGCACAAGGCCCTGTCA
 TCGACATTGGCATGCTAACACAGGAAAGTTATCATGACTGCCTCCAGTGCACACCAGTC
 CTCATCTGGAGCCTGAAGGGTCAAGTGCCTACCATCAACACCAACCAGATGAACAAACAC
 ACACGCTGCTGTATCTCCCTGTGGCAGATTGTAGCCTCGTGTGGCTCACCCAGATGTGA
 AGGTTTGGGAAGTCTGCTTGGAAAGAACAGGGGGAGTCCAGGGAGGTGGTGCAGGCCCTCGAA
 CTAAGGGCCACTCCGGCTGTGCACTCGTTGCTTCTCAACGACTCACGGAGGATGGC
 TTCTGTCTCCAAGGATGGTACATGGAAACTGTGGACACAGATGTGAATACAAGAACAGC
 AGGACCCCTACTTGCTGAAGACAGGCCGTTGAAGAGGCCGGGGTGCAGGCCGTGCCG
 CTGGCCCTCTCCCCAACGCCAGGTCTGGCCTGGCCAGTGGCAGTAGTATTCTATCTCA
 CAATACCCGGCGGGCGAGAACGGAGGTGCCTTGAGCGGGTCCATGGCAGTGTATGCCA
 ACTTGTCTTTGACATCACTGGCCCTTCTGGCCTCCTGTGGGGACCGGGCGGTGCAGGCTG
 TTTCACACACACTCCTGGCCACCGAGGCATGGTGGAGGAGATGCAGGGCACCTGAAGCGGGC
 CTCCAACGAGAGCACCCGCCAGAGGCTGCAGCAGCTGACCCAGGCCAACAGAGACCC
 AGAGCCTGGTGCCTGAAGAACAG**TGA**CTCTGGAGGGCCGGCGCAGAGGATTGAGGAGGAG
 GGATCTGGCCTCTCATGGCACTGCTGCCATTTCTCCCAGGTGGAAGCCTTCAAGAG
 AGTCTCTGGTTCTTACTGGTGGCCTGCTTCTCCCATTGAAACTACTCTTGCTACTT
 AGGTCTCTCTTTGCTGGCTGTGACTCCTCCCTGACTAGTGGCAAGGTGCTTTCTC
 CTCCCAGGCCAGTGGTGGAAATCTGCCCCACCTGGCACTGAGGAGATGGTAGAGAGGAG
 AGGAGAGAGAGAGAGAATGTGATTTGGCCTGTGGCAGCACATCCTCACACCCAAAGAAG
 TTTGTAATGTTCCAGAACACACTAGAGAACACCTGAGTACTAACGAGCAGTTGCAAGGA
 TGGGAGACTGGGATAGCTTCCCCTCACAGAACTGTGTTCCATAAAAAGACACTAAGGGATT
 TCCTTCTGGCCTCAGTTCTATTGTAAGATGGAGAATAATCCTCTCTGTGAACCTTGCA
 AAGATGATATGAGGCTAAGAGAATATCAAGTCCCCAGGTCTGGAAGAAAAGTAGAAAAGAGT
 AGTACTATTGTCCAATGTCAAGAACAGTGGTAAAGTGGAAACCAGTGTGCTTGAAC
 TTAGAAACACATTCTGGAGGCAAGTGGACTTGATCATACATTATATGGT
 TGGGACTTCTCTTCGGGAGATGATATCTGTTAAGGAGACCTTTCAAGTCAAG
 TTCATCAGATATTGAGTGCCCACCTGTGCCAAATAAATGAGCTGGGATTAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK
QYQRIRKEKPQQHNFTHRLLAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFSPDCRAFIWVLANGDTLRFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTVLIWSLGQVLSTINTNQMNNTAAVSPCGRFVASCG
FTP DVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEAAAGAAPCRLALS PNAQVLALASGSSIHLYNTRGEKEECFERVH
GECIANLSFDITGRFLASC GDRAVRLFHNTPGH RAMVEEMQGHLKRASN ESTRQRLQQQLTQ
AQETLKSLGALKK

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTCGCCTCACCCCAAGTGACC**ATG**AGAGGTGCCACCGAGTCTCAATCATGCTCC
 TCCTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGCTGTGAGCAGGGATGTCCAGTGT
 GGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTCGAGGGCTGCGGATGTGCACCCCGCT
 GGGCGGGAAAGGCGAGGAGTGCCACCCCGCAGCCACAAGGTCCCCTTTCAGGAAACGCA
 AGCACCACACCTGTCCTGCTTGCCTAACCTGCTGTGCTCCAGGTTCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATT**TAG**GCCTGCCTGGTCTCAGGATAACCA
 CCATCCTTCTGAGCACAGCCTGGATTTTATTCGCCATGAAACCCAGCTCCATGAC
 TCTCCCAGTCCCTACACTGACTACCCTGATCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTCTCTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCCCTCCCCCAGGTGACCTGCTCTTTCTGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCCGGGCACAGGCTCTGGGT
 GCATTGCTCAGAGTCCCAGGTCTGGCCTGACCTCAGGCCCTCACGTGAGGTCTGTGAGG
 ACCAATTGTGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTAGTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCTCTTACACACTTACCA
 TAACCACGTGAAGCCCCAATTCCCACAGCTTCCATTAAAATGCAAATGGTGGTGGTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTAAACAACCTCTTCCA
 AGGATCAGCCCTGAGAGCAGGTGGTACTTGGAGGAGGGCAGTCCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGCTGAAAGGGGACTGATTGAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTGAATAAAAGCACCAACTGAAAAAA

FIGURE 266

MRGATRVSIMLLLTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHP
GSHKVPFFRKHKHTCPCLPNLLCSRFPDGRYRCSDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

FIGURE 267

AGCGCCCGGGCGTCGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAAATGTCTTTC
 CTCCAGGACCCAAGTTCTCACCATGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGC
 TGCTGCCTTGGCATTGCTGCTGCCAACACAGACGTGTTCTGTCCAAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTCAA
 GCAAAGGAGCTATGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTT
 CCTCTGTCGAGAGGAAGCTGCGGATCTGCCTCCCTGAAAAGCATGTTGGACCAGCTGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTCCAGCCTTAT
 TTCAAAGGAGAAATCTCCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCCGAAGAT
 GATGTTATGGGATTATCCGTCTGGAGTGTTACAACCTCTCCGAGCCTGGAACGGAG
 GCTTCTCTGAAACCTGGAAGGAGAAGGCTTCATCCTGGGGAGTTTCGTGGTGGGATCA
 GGAAAGCAGGGCATTCTCTTGAGCACCGAGAAAAAGAATTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAACGATGATCAAACACAGACTTGGCCTCAGAGAAAAAATGA
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTCATGGGATGTATT
 GTTCCACTCGTGTCCCTAACGGAGTGAGAAACCCATTACTCTACTCTCAGTATGGATT
 TTAATGTATTTAATATTCTGTTAGGCCACTAACGGAAAATAGCCCCAAACAAGACTGA
 CAAAAATCTGAAAAACTAATGAGGATTATTAAGCTAAACCTGGAAATAGGAGGCTTAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTCGGAGTTCGAGACCAAGCCTGAGCAACATGGCGAAACCCGTC
 TCTACTAAAAATACAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTGAACCTGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKAALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEgefILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

FIGURE 269

ACGGACCGAGGGTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCG
 GGCCAGGTGCCCGTCGCAGGTGCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
 AGCCCCTCCTCGCGCTGCCAACCGCCACCCAGCCATGGCGAACCCGGCTGGGCTG
 CTTCTGGCGCTGGCCTGCCGTTCTGCTGGCCGCTGGGGCCGAGCCTGGGGCAAATACA
 GACCACTCTGCAAATGAGAATAGCACTGTTTGCCTCATCCACCAGCTCCAGCTCCGATG
 GCAACCTGCGTCCCGAACGCCATCACTGCTATCATCGTGGTCTTCTCCCTTGGCTGCCTG
 CTCCTGGCTGTGGGCTGGCACTGTTGGTGCGGAAGCTCGGGAGAACGGCAGACGGAGGG
 CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCATGCAGCCGAGGCCGGCCCTCAGG
 ACTCCAAGGAGACGGTGCAGGGCTGCCATCTAGGTCCCCTCCTGCATCTGTCTCC
 CTTCATTGCTGTGACCTGGGAAAGGCAGTGCCCTCTGGCAGTCAGATCCACCCAG
 TGCTTAATAGCAGGAAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG
 GCTATTCACTTTATATATTATAAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAA

270/330

FIGURE 270

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSSSSDGTLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

FIGURE 271

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTATTCCAATAACATTGGGTT
TTGGGATTTAATTTCAAACACAGCAGA**ATG**ACATTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTGGAGATCCAATTAGGAAGCACACATGGAGAATGGCTACTTCT
ATCAAGAAATAAGAGAACCAAGTCAACCCACACAATCATCTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAAACCACAGGCAGGGCATAGTAAAGGACGGAATCTGACTCAAGA
GGGTTAATTCTGGTGCTGAAGCCTGGGCAGGGGTGTAAGAAAAACACT**TAG**ATTCAATG
ATTGTAAATTAAAGGCAAATACACATATTAGTATTACCTAGTGTAAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTAAAATCAGTAACTGATTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTGATACAAATAAAAGAAAAGTGTCTCTCCCCTACAGAATTGACATTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAAA

FIGURE 272

MTFFLSLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWRGVKKNT

ପ୍ରକାଶକ ମେଳିକା

FIGURE 273

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTATTCAAGAGGTTGTTCCCTCTAGTTCT
 GTGCCTGCTGCACCAGTCAAATACTCCTCATTAAGCTGAATAATAATGGCTTGAAGATA
 TTGTATTGTTAGATCCTAGTGTGCCAGAAGATGAAAAAATAATTGAACAAATAGAGGAT
 ATGGTGAACACAGCTCTACGTACCTGTTGAAGCCACAGAAAAAGATTTTTCAAAA
 TGTATCTATATTAACTCCTGAGAATTGGAAGGAAAATCCTCAGTACAAAAGGCCAAACATG
 AAAACCATAAACATGCTGATGTTAGTGCACCACACTCCCAGGTAGAGATGAACCA
 TACACCAAGCAGTCACAGAATGTGAGAGAAGGCAGAATACATTCACTCACCCTGACCT
 TCTACTGGAAAAAAACAAAATGAATATGGACCACCGAGGCAAACACTGTTGTCCATGAGTGG
 CTCACCTCCGGTGGGAGTGTGAGTACAATGAAGATCAGCCTTCTACCGTGCTAAG
 TCAAAAAAAATCGAACAAAGGTGTTCCGAGGTATCTCTGGTAGAAATAGAGTTATAA
 GTGTCAGGAGGCAGCTGCTTAGTAGAGCATGCAGAATTGATCTACAACAAAATGTATG
 GAAAAGATTGTCAATTCTTCTGTATAAAGTACAACAGAAAAGCATCCATAATGTTATG
 CAAAGTATTGATTCTGTTGTAATTGTAACGAAAAACCCATAATCAAGAAGCTCCAAG
 CCTACAAAACATAAAGTGCATTAGTAGTACATGGGAGGTGATTAGCAATTCTGAGGATT
 TTAACAAACACCATACCCATGGTGACACCACCTCCACCTGTCTCTCATGCTGAAGATC
 AGTCAAAGAATTGTTGCTAGTTCTGATAAGTCTGGAAGCATGGGGGTAAGGACCGCCT
 AAATCGAATGAATCAAGCAGCAAACATTCCTGCTGCAGACTGTTGAAAATGGATCCTGG
 TGGGATGGTTCACTTGATAGTACTGCCACTATTGTAATAAGCTAACCTAAATAAGC
 AGTGTGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGAACCTCCAT
 CTGCTCTGGATTAAATATGCATTTCAGGTGATTGGAGAGCTACATTCCAACACTCGATGGAT
 CGAAGTACTGCTGACTGATGGGAGGATAACACTGCAAGTCTTGTATTGATGAAGTG
 AAACAAAGTGGGGCATTGTCATTATTGCTTTGGAGAGCTGCTGATGAAGCAGTAAT
 AGAGATGAGCAAGATAACAGGAGGAAGTCATTGTTATGTTAGCTGAGCTCAGAACATG
 GCCTCATTTGCTTGGGCTCTACATCAGGAAATACTGATCTCTCCAGAACATCCCT
 CAGCTCGAAAGTAAGGGATAACACTGAATAGTAATGCCCTGGATGAACGACACTGTCATAAT
 TGATAGTACAGTGGAAAGGACACGTTCTTCATCACATGGAACAGTCTGCCTCCAGTA
 TTTCTCTGGATCCCAGTGGAAACAATAATGGAAAATTTCACAGTGGATGCAACTTCCAA
 ATGGCTATCTCAGTATTCCAGGAAC TGCAAAGGTGGCACTTGGCATAACATCTCAAGC
 CAAAGCGAACCCAGAAACATTAACATTACAGTAACCTCTCGAGCAGCAAATTCTCTGTGC
 CTCCAATCACAGTGAATGCTAAATGAATAAGGACGTAACAGTTCCCGAGCCAAATGATT
 GTTACCGAGAAATTCTACAGGATATGTAACCTGTTCTGGAGGCAATGTGACTGTTCAT
 TGAATCACAGAATGGACATACAGAAGTTTGGAAACTTTGGATAATGGTGCAGGCCTGATT
 CTTCAAGAATGATGGAGTACTCCAGGTATTTACAGCATATACAGAAAATGGCAGATAT
 AGCTTAAAGTCTGGGCTCATGGAGGAGCAAACACTGCCAGGCTAAATTACGGCCTCCACT
 GAATAGAGCCCGTACATACCAAGGCTGGTAGTGAACGGGAAATTGAAGCAAACCCGCAA
 GACCTGAAATTGATGAGGATACTCAGACCACCTGGAGGATTCAAGCCGAAACAGCATCCGGA
 GGTGCATTGTGGTATCACAAGTCCAAGCCTTCCCTGCTGACCAATACCCACCAAGTC
 AATCACAGACCTGATGCCACAGTTCATGAGGATAAGATTATTCTACATGGACAGCACCAG
 GAGATAATTGATGTTGGAAAAGTCAACGTTATATCATAAGAATAAGTGAAGTATTCTT
 GATCTAAGAGACAGTTGATGATGCTCTCAAGTAATACTACTGATCTGTACCAAAGGA
 GGCAACTCCAAGGAAAGCTTGCATTAAACCAAGAAAATATCTCAGAAGAAAATGCAACCC
 ACATATTATTGCAATTAAAGTATAGATAAAAGCAATTGACATCAAAGTATCCAACATT
 GCACAAAGTAACCTGTTATCCCTCAAGCAAATTCTGATGACATTGATCTACACCTACTCC
 TAATCCTACTCCTACTGATAAAAGTCATAATTCTGGAGTTAATATTCTACGCTGGTAT
 TGTCTGTGATTGGGCTGTTGTAATTGTTAATTCTGTTATTGAGTACCACTT**TGA**ACCTTA
 ACGAAGAAAAAAATCTCAAGTAGACCTAGAAGAGAGTTAAAAACAAAATGTAAGT
 AAAGGATATTCTGAATCTAAAATCATCCCATGTGATGACATCAAACACTCATAAAAATAATT
 TTAAGATGTCGGAAAAGGATACTTGTATTAAATAAAAACACTCATGGATATGAAAAACTGT
 CAAGATTAAATTAAAGTTCATTATTGTTATTGAGTAAAGAAATAGTGAAC
 AAAGATCCTTTCTACTGATACCTGGTTGATATTGATGCAACAGTTCTGAAAT
 GATATTCAAATTGCAAGAAATTAAATCATCTGAGTAGTCAAACAAACAGTAA
 GGAGAGCAAATAAACACATTGGAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

FIGURE 274

MGLFRGFVFLVLCLLHQSNSTFIKLNNGFEDIVIDPSVPEDEKIIIEQIEDMVTTASTY
LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPTLPGRDEPYTKQFTEC
GEKGEYIHFTPDLLLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
CSAGISGRNRVYKCQGGSCLSACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVE
FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLLKISQRIVCLV
LDKSGSMGGKDRLNRMNQAAKHFLIQTVENGSWGMVHFSTATIVNKLIQIKSSDERNTLM
AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLTDGEDNTASSCIDEVKQSGAIVH
FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPG
TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNDVNSFPSPMIVYAEILQG
YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDGVYSRYFTAYTENGRLKVRAHG
GANTARLKLRRPPLNRAAYIPGWVNNGEIEANPPRPEIDEDTQTTLEDTSRTASGGAFVVSQV
PSLPLPDQYPPSQITDLDATVHEDIILTWTAPGDNFDVGVQRYIIRISASILDLRDSFDD
ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIP
QANPDDIDPTPTPTPDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTAGGTGGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATAACGTCCCCG
 GGCAGGGGTGACAACAGGTGTCATCTTTGATCTCGTGTGGCTGCCTCCTATTCAAGGAAAG
 ACGCCAAGGTAACTTGACCCAGAGGAGCAATGATGTAGCCACCTCTAACCTCCCTCTGAACC
 CCCAGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTCGGCTTAACCT
 GTGGTTGGAGGAGAGAACCTTGTGGGCTGCGTTCTTAGCAGTGTCAAGAAGTGACTTGCCTGA
 GGGTGGACAGAAGAAAGGAAAGGAAAGGCTCCCTCTGTGTGGCTGCACATCAGGAAGGCTGTGATGGG
 AATGAAGGTGAAAACCTGGAGATTCTACTGATCTAGCTATTGCTCTGCCTGCAAGATCATCCTTAAAAA
 GTAGAGAAGCTGCTGTGTGGTTAACTCCAAGAGGAGCAACTCGTTAGAAGGAAATGGATG
 CAAGCAGCTCCGGGGCCCCAAACGCATGCTTCTGTGGTAGGCCAGGGAAGCCCTCCGTGGGG
 GCCCGGCTTGAGGGATGCCACCGGTCTGGACGCATGGCTGATTCTGA**ATG**ATGATGGTTGCC
 GGGGGCTGCTTGCCTGGGATTTCCGGGTTGGTTTGCTGGTGTCTCTCTGCTGTGCTATCTCTGT
 CCTGTACATGTTGGCCTGCAACCCAAAAGGTGACGAGGAGCAGCTGGCACTGCCAGGGCCAACAGC
 CCACACGGGAGGGGGTACAGGCCCTCAGGAGTGGGAGGAGCAGCACCGCAACTACGTGA
 GCAGCCTGAAGCGGAGATGCCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGGAA
 TGGCAGTACCAAGCCAGCGATGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAG
 GCCGACCTCTGGCCTTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCTCAAGCTGG
 CCACAGAGTATGCAGCAGTGCCTTGCATAGCTTACTCTACAGAAGGTGTACAGCTGGAGACTGG
 CCTTACCCGCCACCCGAGGAGAAGCCGTGTGAGGAAGGACAAGCGGGATGAGTTGGTGAAGGCCATT
 GAATCAGCCTGGAGAACCTGCAACATCTGCAGAGAACAGCCCCAATCACCGTCTTACACGGCCCT
 CTGATTTCATAGAAGGGATCTACCGAACAGAAGGGACAAAGGGACATTGTATGAGCTCACCTTCAA
 AGGGGACCAACACGAATTCAAACGGCTCATCTTATTTCGACCATTAGCCCATCATGAAAGTG
 AAAATGAAAAGCTAACATGGCAACACGTTATCAATGTTATCGTGCCTCTAGCAAAAGGGTGG
 ACAAGTTCCGGCAGTTCATGCAGAATTTCAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCT
 CACTGTTGTTACTTGGGAAAGAAGAATAAATGAAAGTCAAAGGAATACTGAAAACACTTCCAAA
 GCTGCCAACTTCAGGAACCTTACCTTCATCCAGCTGAATGGGAAAGGAAAGGGACTTCTGGGGAAAGGGACTTG
 ATGTTGGACCCGCTCTGGAAAGGGAGCAACGCTCTCTTCTGTGATGTGGACATCTACCTT
 CACATCTGAATTCTCAATACGTGTAGGCTGAATACACAGCCAGGGAGAAGGTTATTTATCCAGTT
 CTTTCAGTCAGTACAATCTGGATAATACAGGCCACCATGATGCAGTCCCTCCCTGGAACAGC
 AGCTGGTCATAAAGAAGGAAACTGGATTGGAGAGACTTGGATTGGATGACGTGTCACTG
 GTCAGACTTCATCAATATAGGTGGGTTGATCTGGACATCAAAGGCTGGGGGGAGAGGATGTGCAC
 CTTTATCGCAAGTATCTCCACAGCAACCTCATAGTGGTACGGACGCGCTGTGCGAGGACTCTCCACC
 TCTGGCATGAGAACGCCTGCATGGACGAGCTGACCGGGAGCAGTACAAGATGTGCATGCAGTCCAA
 GGCCATGAACGAGGACATCCCACGGGAGCTGGCATGTTGAGCAGGAGATAGAGGCTCAC
 CTCGCAAACAGAACAGAACAGTAGCAAAAAACAT**TGA**ACTCCCAGAGAAGGATTGTGGAGA
 CACTTTCTTCTTGTCAATTACTGAAAGTGGCTGCAACAGAGAAAAGACTCCATAAAGGACG
 ACAAAAGAATTGGACTGATGGGTAGAGATGAGAAAGCCCTCGATTCTCTGTGTTGGCTTTAC
 AACAGAAATCAAATCTCCGTTGCTGCAAAGTAAACCGAGTGGCAGCTGTGAAGTGTCTGACA
 AAGGCAGAAATGCTGTGAGGATATAAGCTAATGGTGTGGAGGTTTGATGGTGTAAATACACT
 GAGACCTGTTGTTGTGCTCATGAAATATTCTCATATGAATGAGCCTATCAGCAGGGCTCTAGTTCTAGG
 TAGCATGAAAGGCAAGCATATTCTCTCATATGAATGAGCCTATCAGCAGGGCTCTAGTTCTAGG
 AATGCTAAATATCAGAAGGCAGGAGAGGAGATAGGTTATTATGATACTAGTGAGTACATTAGTA
 AAATAAAATGGACCAGAAAAGAAAACCATAAATATCGTGTCAATTCTCCCAAGATTAAACCA
 AAAATAATCTGTTATCTTTGGTTGCTCTTAAACTGTCCTCGTTTTCTTTATTTAAATTA
 GCACCTTTCTCCCTGTGAGTTAGTCTGCTTAACTTAAATTACCATTTGCAAGCCTACAAGAGA
 GCACAAAGTGGCCTACATTATTTAAATAAGGATACTTTGAGATGCATTATGAGAAACTTCA
 GTTCAAAGCATCAAATTGATGCCATATCCAAGGACATGCCAAATGCTGATTCTGTGAGGCACTGAAT
 GTCAGGCATTGAGACATAGGGAAGGAATGGTTGACTAATACAGACGTACAGATACTTCTCTGAA
 GAGTATTTCGAAGAGGAGCAACTGAACACTGGAGGAAAGAAAATGACACTTCTGCTTACAGAA
 AAGGAAACTCATTCAAGACTGGTGTACCTAAAGTCAGAAACACATTCTCCCTCA
 GAAGTAGGGACCGCTTCTTACCTGTTAAATAAAACCAAGTACCGTGTGAACCAAACATCT
 TTCAAAACAGGGTGTCTCTCTGGCTCTGGCTTCCATAAGAAGAAATGGGAGAAAATATATAT
 ATATATATATATTGTGAAAGATCAATCCATCTGCCAGAATCTAGTGGATGGAAGTTTGCTACAT
 GTTATCCACCCAGGCCAGGTGGAAAGTAACGAAATTATTAAATAAGCAGTCTACTCAATCA
 CCAAGATGCTTCTGAAAATTGCAATTACCATTTCAAACATTTTTAAATAAAACATCAGTA
 ACATAGAGTGGTTCTCATGTGAAAATTATTAGCCAGCACCAGATGCATGAGCTAATTATCT
 CTTGAGTCCTGCTTGTGCTCACAGTAAACTCATTGTTAAAAGCTTCAAGAACATTCAAGC
 TGTTGGTGTGTTAAAAATGCATTGTATTGATTGACTGGTAGTTATGAAATTAAATTAAACAC
 AGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAAATGATTGTTGAGTAA

FIGURE 276

MMMVRRGILLAWISRVVVLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVPFDSTLQKVYQLETGLTRHPEEKPVRKDKRDELVEAIESALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYLETFKGDHKHEFKRLILFRPFSPIMKVNEKLNMANTLINVIVPLAKRVDKFRQFMQNREMCEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSQYNPGIIYGHDAVPPLEQQLVIKKETGFWRDFGFGMTQCYRSDFINIGGFDLIDIKWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPEQYKMCMQSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

FIGURE 277

GAAAGA**ATG**TTGTGGCTGCTTTCTGGTACTGCCATTGCTGAACCTGTCAACC
 AGGTGCAGAAAATGCTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCAT
 ATGCCTGGGATACCAATGAAGAACACCTCTCAAAGCGATGGTAGCTTCTCCATGAGAAA
 GTTCCAACAGAGAACAGAAATTCCCAGTCCTACTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTGTGGTTACAGACCCCTCAAAAATCACACCCTCTGCTGTTGAGGTGC
 AATCAGCCATAAGAACATGAACAAGAACCGGATCAACAATGCCTCTTCTAAATGACCAAAC
 CTGGAATTTAAAAATCCCTCCACACTGCACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATTTGGTGTGATATTCATCATCATAGTTGCAATTGCACTACTGATTAT
 CAGGGATCTGGCAACGTAGAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTAAAACATGATCACAATTGAAAATGGCATCCCTCTGATCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCTCA**TGA**CAGAGGATGAGAGGCTCACCCCTCTGAAGGGCTGT
 TGTTCTGCTCCTCAAGAAATTAAACATTGTTCTGTGTGACTGCTGAGCATCCTGAAATA
 CCAAGAGCAGATCATATATTTGTTACCATTCTCTTGTAAATAATTGAAATGTGCT
 TGAAAGTGAAAAGCAATCAATTACCCACCAACACCACTGAAATCATAAGCTATTACGAC
 TCAAAATATTCTAAAATATTTCTGACAGTATAGTGTATAATGTGGTATGTGGTATTG
 TAGTTATTGATTAAAGCATTTAGAAATAAGATCAGGCATATGTATATATTTCACACTTC
 AAAGACCTAAGGAAAATAAATTCCAGTGGAGAACATATAATATGTGTAGAAATCAT
 TGAAAATGGATCCTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
 TGAGAAGTAATTATTGTAATGGATGGATAAAATGGAATTACTCATATACAGGGTGGAAATT
 TTATCCTGTTATCACACCAACAGTTGATTATATTTCTGAATATCAGCCCCTAATAGGAC
 AATTCTATTGTTGACCATTCTACAATTGAAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 278

MLWLLFFILVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NCREATEISHVLLCNVTQRVSFWFVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLE
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLLILSGIWQRRRNKEPSEVDDAEDKC
ENMITIENGIPSPLDMKGGLMMPS

© 2009 SAGE Publications
10.1177/0886260509339222
<http://jep.sagepub.com>
Downloaded at 12:15 21 December 2013

FIGURE 279

AACTCAAACCTCTCTGGAAAACGCGGTGCTTGCTCCTCCGGAGTGGCCTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCGTCCGGTCTCTGGGCCAAGGCTGGGTTCCCTC**ATGT**
 ATGGCAAGAGCTACTCGTGCAGTCTCTGGCATACAGCTCACAGCTCTTGG
 CCTATAGCAGCTGTGGAAATTATACTCCGGTGCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAAATGCACTTCTCCAGCTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTCTGCCTCTAGACGGGGGACCTGAGCAGTTGTATTCTACTACCACATAGATCCCTC
 CAACCCATGAGTGGCGGTTAAGGACCGGGTCTGGATGGAATCCTGAGCGGTACGA
 TGCCTCCATCCTCTGGAAACTGCAGTCGACGACAATGGGACATAACACTGCCAGGTGA
 AGAACCCACCTGATGTTGATGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTGAGATCCACTCCTGGCTCTGGCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTTAGTGGCCTCTCCAGCATTACCGAAAAAGCGATGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTAGAAGACACAGACT**TAA**CAATTAGATGGAAGCTGAGATGATTCCAAGAACAA
 GAACCTAGTATTCTTGAAGTTAATGGAAACTTTCTTGGCTTCCAGTTGACCCGT
 TTTCCAACCAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTATTTAATTCA
 GTGTAATTTCAAGTGCCTAGGTTTATAAACAGAAGCTACATTTGCCCTTAA
 GACACTACTACAGTGTATGACTTGTATACACATATATTGGTATCAAAGGGATAAAAGCC
 AATTGCTGTTACATTCCTTCACTGATTCTCAATTAAAGGTGAGCTAACGCTCCTCGGT
 ATGTGTTACTCTCTTCCCACATTCTCAATTAAAGGTGAGCTAACGCTCCTCGGT
 TTTCTGATTAACAGTAAACTCAAACGTTAAATGACATTTCATATTCCAGGTGATAGATT
 TCCTTAACATGAGACACATCTGTTACTGAATTCTTCAATATTCCAGGTGATAGATT
 TTTGTGCG

FIGURE 280

MYGKSSTRAVLLLGIQLTALWPIAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTWT
WNFRPLDGGPEQFVFYYHIDPFQPMSGRFKDRVSDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLFQHYRKKRWAER
AHKVVEIKSKKEERLNQEKKVSVYLEDTD

FIGURE 281

GCATTTTGTCTGTGCTCCCTGATCTCAGGTACCCACCATGAAGTTCTAGCAGTCCTGGT
ACTCTGGGAGTTCCATCTTCTGGTCTCTGCCAGAACATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCAC TGCTGCT
GCAACCAC T GCG ACC ACT GCT GCT CCT ACC ACT GCA ACC ACC GCT GCT T CT ACC ACT GCT CG
TAAAGACATTCCAGTTACCCAAATGGGTTGGGATCTCCGAATGGTAGAGTGATGCTCCCT
GAGATGGAATCAGCTTGAGTCTTGCAATTGGTCACAACATTCTCATGCTTCTGTGATTTC
ATCCAAC T ACTTACCTTG C CT AC G AT AT CCC C TT AT CT CTA AT CAG TT AT TT CTTCAA
ATAAAAATAACTATGAGCACATAAAAAAAAAAAAAA

FIGURE 282

MKFLAVLVLLGVSIIFLVSQNPPTAAPADTYPATGPADDEAPDAETTAATTATTAAAPTTAT
TAASTTARKDIPVLPKWVGDLNGRVCP

FIGURE 283

GGACTCTGAAGGTCCAAGCAGCTGCTGAGGCCCAAGGAAGTGGTCCAACCTGGACCC
CTAGGGGTCTGGATTGCTGGTTAACAGATAACCTGAGGGCAGGCACCCATAGGGGA**ATGC**
TACCTCCTGCCCTCCACCTGCCCTGGTGGTACGGTGGCCTGGTCCCTCCTGCCGAGAGA
GTGTCTGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTGTTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGG
GACAGTTCTGTTGTGCTTGGTGGACAGTAAGAGGGCTTGGCCAGTCCAGGGTGGGGGCG
GCAAACCTCCATAAAGAACAGAGGGCTGGGCCACAGAGTCATCTGCCAGCTCCT
CTGCTGCCAGTGGAGTGGCACGAGGTGGGCTTGTGCCAG**TAA**AACCACAGGCTGG
ATTTGCCTGCCAGTGGAGTGGCACGAGGTGGGCTTGTGCCAG**TAA**AACCACAGGCTGG
CCCCAAAGAGCTTCATTGTATCTATTGATTTCACACATTAGCAATTAAAAGTGA
GGGCCGGGCACGGTGGCTACGCCTGTAATCCCAGCACTTGGGAGGCCAGGGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCAACATGGTGAACCTTGTCTACTAAAAA
TACAAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGCGACAAGAGTGAGACTCCATCTCACACA

284/330

FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHLRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLLCCWPVGVARGGALCQ

FIGURE 285

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
 GCGGCCCATGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTTTCCATGG
 GACCCTGCAGCTGGGCCAGGCCCTCAACGGTGTACAGGACCACGGAGGGACGGCTGACAA
 AGGCCAGGAACAGCCTGGGTCTCTATGCCGCACAATAGAACTCCTGGGGCAGGAGGTAGC
 CGGGGCCGGGATGCAGCCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
 TATTCTGCAGCTGCAGGCAGGCCACAGCTGAGGTGCTGGGGAGGTGGCCAGGCACAGA
 AGGTGCTACGGACAGCGTGCAGCGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGCCCT
 GCCTACCGAGAATTGAGGTCTAAAGGCTACGCTGACAAGCAGAGCCACATCCTATGGC
 CCTCACAGGCCACGTGCAGCGCAGAGGCGGGAGATGGTGGCACAGCAGCATGGCTGCGAC
 AGATCCAGGAGAGACTCCACACAGCGCGCTCCAGCCTGAATCTGCCTGGATGGAACGTGAG
 GACCAATCATGCTGCAAGGAACACTTCCACGCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
 CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
 GCAGGCAGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
 CCCTTCATGCCTACACACCCCTCATTAAAGCAGAGTCGTGGCATTCAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRLT
ARNSLGLYGRТИELLGQEVSRRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ
IQERLHTAALPA

FIGURE 287

GGCAACATGGCTCAGCAGGCTGCCAGAGCCATGGCAAAGAATGGACTTGTAAATTGCAT
 CCTGGTGATCACCTTACTCCTGGACCAGACCAGCCACACATCCAGATTAAAGCCAGGA
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
 TGGACAGAAGTCAATGCCTGAAGGAAATTCAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTCACAAGAAATGCTACCTGCTCAGAAGGTTGAAGCATTCCATGAGGCCAATG
 AAGACTGCATTCCAAGGAGGAATCCTGGTTATCCCCAGGAACCTCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTGGCTGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTGTTGACGTCAACGGAATCGCTATCTCCTCCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAATGTGTCCTGTTCTCCAATCAGCTCAG
 GGCAAGTGGAGTGTGAGGCCCTGTCGCAGCAAGAGATAACATATGCGAGTTCACCATCCC
 TAAATAGGTCTTCTCAAATGTGTCCTCCAAGCAAGATTCACTACATAACTTATAGGTTATGA
 TCTCTAAAGATCAAGTAAAAATCATAATTTTACTTATTAAAAAATTGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTGCTAACACATTCTTGGGATTTGCCCT
 TCCTGGGTATAGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTCTGCT
 AAACAGACTAAAATCTTCTCTAGTCTTCACTGTACAAACCCAGTTGTTCAA
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGGAGTTAGCGTATGTTGACTAACAAAAATTCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAATTTCACTGCCTGTCATTCTGTCCATGCTGGCAATAATACC
 TTGTCAGCCCATTACCCATTGGAAATTGCTCCATCTCCTGGTGGACTTGTATCTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTGATTTTTTTCTCATGCC
 TACCCCTTTGGAGTTCCAGCCGAATTGAAATGACAAGGTGTATATTGAT
 CAATTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGTAACCCCTAAGGCATAT
 CAAAGAACGATTGCATGATAAACGGAAATAGAAAAAGAACCTACATTATTTGCTTT
 AGCATCCTTACTCTCACCTTATGAGATTGAGAGTGGACTTACATTCTTTTACATT
 TCGTATATTATTAGCCATTATGTTAAAGAATGCTATCTGGAAAATTGCATACGTCTGTGCAATT
 TGGAAAGCTGAAAATGAAATTAAAGAATGCTATCTGGAAAATTGCATACGTCTGTGCAATT
 TTTTATTCTGCCTAGTGCTATTCTGCTTAACTAGATTGACAAATAACTCATTGCT
 TAATATCAAATTACAAAGTTAGACTTGGAGGGAAATGGCTTTAGAAGCAAACAATT
 AAATATATTGTTCTCAAATAAATAGTGTAAACATTGAATGTGTTGTGAACAATT
 CCCACTTGCAAACCTTAACACATGCTGGAATTAAGTTTAGCTGTTTCAATTGCTCA
 ATAATAAAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAA

FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLQDQTSHTSRLKARKHSKRRVRDKDGDLKTQIEKLWT
EVNALKEIQALQTVCLRGTVKHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQGK
WSDEACRSSKRYICEFTIPK

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTGCCCGGGCAGCCGCAGGTTCCCCGCGC
CCCGAGCCCCCGCGCCATGAAGCTCGCCGCCCTCCTGGGCTCTGCGTGGCCCTGTCCCTGCA
GCTCCGCTGCTGCTTCTTAGTGGCTCGGCCAACGCTGTGGCCAGCCTGTCGCTGCGCTG
GAGTCGGCGGGAGGCCGGGGACCCCTGGCCAACCCCCCTGGCACCCCTAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGTCCCCAGGCCGTGGGGCGTGAAGGCCCTGAAGGCCCTGCTGGG
GCCCTGACAGTGTTGGCTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCCGAGGGCTGAAAACCCGCCGCCGGGAGGACCGTCCATCCCCTCCCCGGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

290/330

FIGURE 290

MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLS
SLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTIVFG

FIGURE 291

TGAAGGACTTTCCAGGACCAAGGCCACACACTGGAAGTCTGCAGCTGAAGGGAGGCACT
 CCTGGCCTCCGAGCGATCAC **ATG**AAGGTGGTGC~~C~~AAAGTCTCCTGCTCTCCGTCCTCCTG
 GCACAGGTGTGGTACCGGCTGGCCCCAGTCCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAACAGACCAGCAGGGTAGTCAGGCTCCAGGGAGGAAGAGAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTAGGAAAGAGAAGCCTGGCTGATGCCAGCAGCAGCTT
 GCCAAGGAGACTCAAACCTCGGATTCAGCCTGCTGCCAAAGATCTCATGAGGCACGATGG
 CAACATGGTCTCTCCATTGGCATGTCCTGGCATGACAGGCTTGATGCTGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTGCAGGCCCTGAAGCCCACCAAG
 CCCGGGCTCCTGCCTCCCTTAAGGGACTCAGAGAGACCCCTCCCGAACCTGGAAC
 GGGCCTCTCACAGGGAGTTGCCTCATCCACAAGGATTTGATGTC~~AA~~AGAGACTTTCT
 TCAATTATCCAAGAGGTATTTGATACAGAGTGC~~G~~C~~T~~C~~T~~ATGAATTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGAAAATTCCAAACT
 GTTTGATGAGATTAATCCTGAAACCAAATTAAATTCTTGTGGATTACATCTTGTCAAAGGGA
 AATGGTTGACCCATTGACCC~~T~~GTCTTCACCGAAGTCGACACTTCCACCTGGACAAGTAC
 AAGACCATTAAGGTGCCATGATGTACGGTGCAGGCAAGTTGCCTCCACCTTGACAAGAA
 TTTCGTGT~~C~~ATG~~C~~C~~T~~CAA~~A~~CTGCC~~T~~ACCAAGGAATGCCACCATGCTGGTGGCCTCA
 TGGAGAAAATGGGTGACCACCTGCC~~T~~GAAGACTAC~~T~~GACCACAGACTGGTGGAGACA
 TGGCTCAGAAACATGAAAACCAGAAACATGGAAGTTCTTCCGAAGTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTCTCACCC~~T~~TG
 CTGACCTTAGTGA~~A~~CTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGACTGAGGCAGTGGCAGGAATCTGTCAGAAATTAC
 TGCTTATTCCATGCC~~T~~GT~~C~~ATCAAAGTGGACCGGCCATT~~C~~ATTTGATCTATGAAG
 AACCTCTGGAATGCTCTGGCAGGGTGGTGAATCCGACTCTCCTA **TAA**TT~~C~~AGG
 ACATGCATAAGCATTG~~C~~TG~~C~~TG~~T~~AGATGCTGAATCTGAGGTATCAAACACACAGGA
 TACCAGCAATGGATGGCAGGGAGAGTGTCTTTGTTCTTA~~A~~CTAGTTAGGGTGTCTC
 AAATAAA~~T~~ACAGTAGTCCC~~A~~TTCTGAGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGCTGAAC~~C~~TTATATATT~~T~~TC~~T~~ACACATACATAC~~T~~ATGAT
 AAAGTTAATTATAAATTAGGCACAGTAAGAGATTAACAATAACAACATTAAGTAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAA~~A~~CTGATTATAGAGAAGGCTA
 CTAAGTGA~~C~~TCATGGCGAGGAGCATAGACAGTGTGGAGACATTGGCAAGGGGAGAATTCA
 CATCCTGGTGGACAGAGCAGGACGATGCAAGATTCC~~C~~ACTACTCAGAATGGCATGC
 TGCTTAAGACTTTAGATTGTTATTCTGGAATTTCATTTAATGTTTG~~G~~ACC~~T~~GGT
 TGACC~~A~~GGTTA~~A~~CTGAGACTGCAGAAAG~~A~~CCATGGATAAGGGAGGACTACTACAAAAA
 GCATTAATTGATA~~C~~ATATT~~T~~AAAAAAAAAAAAAA

FIGURE 292

MKVVPSLLLSQLAQLWVPLAPSPQSPETPAPQNQTSRVVQAPREEEDEQEASEEKAGE
EEKAWLMASRQQLAKETSNGFSLLRKISMHDGNMVFSPFGMSLAMTGLMLGATGPTETQI
KRGLHLQALKPTKPGLLPSLFKGRLRETLSRNLELGLSQGSFAFIHKDFDVKETFFNLSKRYF
DTECVPMNFRNASQAKRLMNHYINKETRGKIPKLFDEINPETKLILVDYILFKGKWLTPFDP
VFTEVDTFHLDKYKTICKVPMMYGAGKFASFDKNFRCHVLKLPYQGNATMLVVLMEMKGDHL
ALEDYLTDLVETWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIRRIIFSPFADLSELSA
TGRNLQVSRLRRTVIEWDERGTEAVAGILSEITAYSMPPVIKVDRPFHFMUYEETSGMLLF
LGRVVNPTLL

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTACAGAGACGCCGGACCCCAGAC**ATGAG**
GAGGCTCCTCCTGGTCAACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTTCCC
TGTCCAGAACGCCGAAACTCTTGACCAACCGAGGGAGAACGCCACGAGGTCAAGGCAGGGGCC
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGAACCCCTGGGCCGTGTGAGTCCC
GAGCCCGACCATGACAGCCTGTACCACCCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAAGGTGCTCCTGGACCGAGGAAGACCAAGACCACA
TCTACCACCCCCAG**TAG**GGCTCCAGGGGCCATCACTGCCCGCCCTGTCCCAGG
CTGTTGGGACTGGGACCCCTCCCTACCCCTGCCAGCTAGACAAATAACCCAGCAGGCAA
AAAAAAAAAAAAAAA

FIGURE 294

MRRLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKA
GARVVEPPEKDDQLVVL
FPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSL
YHPPPEEDQGEE
RPRLWVMPNHQVLLGPEEDQDHLYHPQ

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTG
 TACCCAAGGAAAGTCAGCTGAGACTCAGACAAGATTACA**ATG**AACCAACTCAGCTTCCTGC
 TGTTTCTCATAGCGACCACCAAGAGGATGGAGTACAGATGAGGCTAATACTTACTCAAGGAA
 TGGACCTGTTCTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
 TAGTGCATTTGATGGCCTGTATTTCTCCGACTGAGAATGGTGTATCTACCAGACCTTCT
 GTGACATGACCTCTGGGGTGGCGCTGGACCCCTGGTGGCCAGCGTGATGAGAATGACATG
 CGTGGGAAGTGCACGGTGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTGGATCTGCAGAGGCGGCCACGAGCG
 ATGACTACAAGAACCCCTGGCTACTACGACATCCAGGCCAAGGACCTGGCATCTGGCACGTG
 CCCAATAAGTCCCCATGCAGCACTGGAGAACAGCTCCCTGCTGAGGTACCGCACGGACAC
 TGGCTTCCTCCAGACACTGGACATAATCTGTTGGCATCTACCAGAAATATCCAGTGAAAT
 ATGGAGAAGGAAAGTGGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTGGC
 GACGCCAGAAAACAGCATCTTATTACTCACCCATGGCCAGCGGGAAATTCACTGCAGGGATT
 TGTTCAGTCAGGGTATTAATAACGAGAGAGCAGCCAACGCCCTGTGCTGGAATGAGGG
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTCCAGAGGCCAGT
 CCCCAGCAGTGTGGAGATTTCTGGTTTGATTGGAGTGGATATGGAACTCATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGT**TGA**GAGTTTG
 GGAGGGAAACCCAGACCTCTCCCTCCAAACCATGAGATCCAAGGATGGAGAACAACTTACCC
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLFLIAATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGGWTILVASVHENDMRGKCTVGDRSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGECKCWTDNGPVI PVVYDFGDAQKTASYYSPYGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
FYR

FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGCATCCTGCCCTCGGAACA**ATG**GGACTCGGCGCGAGGTGCTGGGCCG
 CGCTGCTCCTGGGACGCTGCAGGTGCTAGCGCTGCTGGGGCCGCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACACTCCAGTGCTAACTAAC
 AGAGACTCTCCAACATGTGCCCTTGACCATAACAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTACCCACCATGAAACCTACAGCG
 GCATCTAATACAACACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTAAAGTC
 TACACCCAAAACAACAAAGTGTTCACAGAACACATCTCAGATATCACACATCCACAATGACCG
 TAACCCACAATAGTTCACTGACATCTGCTGCTTCATCAGTAACAATCACAACAACTATGCAT
 TCTGAAGCAAAGAAAGGATCAAAATTGATACTGGGAGCTTGTGGTATTGTATTAAC
 GCTGGGAGTTTATCTATTCTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
 GGTATCGAACCATAGATGAACATGATGCCATCATT**TAA**GGAAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAAATTGGTTATTAATAGTTAAAACAATATTCT
 CTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
 AAGATTCTCAAGGTAAACAAGGGTTGGGTTTGAAATAAACATCTGGATCTTAGACCGT
 TCATACAATGGTTTAGCAAGTTCACTGAAAGACAAACAAGTCCTATCTTTGGCT
 GGGGTGGGGCATGGTCACATATGACCAGTAATTGAAAGACGTCACTGAAAGACAGAA
 TGCCATCTGGCATACAAATAAGAAGTTGTACAGCACTCAGGATTTGGTATCTTGT
 AGCTCACATAAAGAACTTCAGTGCTTTCAGAGCTGGATATATCTTAATTACTAAATGCCACA
 CAGAAATTATAACAAACTAGATCTGAAGCATAATTAAAGAAAAACATCAACACATTGG
 TGCTTAAACTGTAGTAGTTGGTCTAGAAACAAACTCC

FIGURE 298

MGLGARGAWAALLGTLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMVTNHSSVTSAASSVTITTMHSEAKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSSRRGIRYRTIDEHDAII

FIGURE 299

CAGCCGGGTCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCGAGCCGGAGCCGG
 TCGCGGGGGCTCCGGCTGTGGACCGCTGGCCCCAGCG**ATG**GCGACCCTGTGGGGAGGC
 CTTCTTGGCTTGGCTCCTGCTCAGCCTGTCGTGCCTGGCGCTTCCGTGCTGCTGCTGGC
 GCAGCTGTCAGACGCCAAGAATTGAGGATGTCAGATGTAATGTATGCCCTCC
 ATAAAAGAAAATTCTGGCATATTTATAAAAGAACATATCTCAGAAAGATTGTGATTGCCCT
 CATGTTGGAGCCATGCCTGTGCGGGGGCCTGATGTAGAACGATACTGTCTACGCTGTGA
 ATGCAAATATGAAGAAAGAACGCTCTGTCACAATCAAGGTTACCATTATAATTATCTCTCCA
 TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTGAGCCCATACTGAAGAGG
 CGCCTCTTGGACATGCACAGTTGATAACAGAGTGATGATGATATTGGGATCACCAGCCTT
 TGCAAATGCACACGATGTGCTAGCCGCTCCCGAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTGACCGG
 CATGTTGCCTCAGC**TAA**TTGGAAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAAGAACTGACTGGGTTTGCTGGTTTCATTTAACCTTGTGATTTTACCAACT
 GTTGCTGGAAGATTCAAAACTGGAAGCAAAACTTGCTTGATTTTTCTTGTAAACGTA
 ATAATAGAGACATTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTCTATTG
 TGACTTTACTAATAAAAATCTGCCTGAAATTCTTGAAGTCCTTACCTGGAACA
 AGCACTCTCTTCAACCACATAGTTAACTTGACTTCAAGATAATTTCAGGGTTTG
 TTGTTGTTGTTTTGTTGTTGGTGGAGAGGGAGGGATGCCTGGAAAGTGGTT
 AACAACTTTTCAAGTCACTTACTAAACAAACTTTGTAATAGACCTACCTCTATT
 TCGAGTTTCATTATTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTG
 ACTTTGCACTGACTGTATTATCTGGGTATCTGCTGTCTGCACTTCATGGTAAACGGGAT
 CTAAAATGCCTGGTGGCTTTCACAAAAAGCAGATTCTTCATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAAACTGCCATTGCTAGTTACTCTAAAGACTAAACATAGTCTG
 GTGTGTGGTCTTACTCATCTTAGTACCTTAAGGACAACCTAAGGACTTGGACACT
 TGCAATAAAAGAAATTATTTAAACCCAAGCCTCCCTGGATTGATAATATACACATTG
 TCAGCATTCCGGTGTGGTGGCTCTTGAAAGGTCTAACCTATTGGATAACTGGCTTTGA
 AGGGCTGGGTTGTGGTGCCTCTGAAAGGTCTAACCTATTGGATAACTGGCTTTGA
 ACTTCCATGTCCCTTTGGAATGTAACAATAAAATAATTGAAACATCAA

300/330

FIGURE 300

MATLWGGLRLGSLLSCLALSVLLAQLSDAAKNFEDVRCKCICPPYKENSGHIYNKNIS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSVTIKVTIIYLSILGLLLLYMYLTL
VEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDLARSRSRANVLNKVEYAQQQRWKLQVQEQQ
RKSVFDRHVVLS

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTC**ATG**GCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTGTCTGGCTCTGTCGCTGCTGCCAAGGCCTCCTGTCGGCGGGAAAGCGG
CAGGAGCCGCCGCGCACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA
CCAGGCACCCCTCAGATGCCAGACTCCTGGGCTCGTTCCAGAGGTCTCACCTGCCGAGG
CATTGCAAAGGCCAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAAGAGGTCTG
ATGGGGCAGATTATTCAAATCTACGGTTTGGGATTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAACATCCTAATCATATTACATCAA**TGA**AAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAACCTTCTTATAGTTCATAAAATTATTCAAATCCATCATCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTCAGTTCACATAAGAATG
TTTACTCAATGTTAAGTGTGCCCCAAAATTACAACAAACAAGGCAGAACTAGGACTT
GAACATGGATCTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

FIGURE 302

MAYSTVQRVALASGLVLALSLLPKAFLSRGKRQEPPPTPEGKLGRFPPMMHHQAPSDGQT
PGARFQRSHLAEAFAKGSGGAGGGSGRGLMGQIPIYGFGLFLYILYILFKVSRIILI
ILHQ

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGAGATTCAGTGCATTGCCCTCCCTGGGTGCTTCATCTT
 GGATTGAAAGTTGAGAGCAGC**ATG**TTTGCCCCTGAATGACTGAATGTTCCCCGCCTGAGCTAACAGTCATGTG
 TGGATTATTCTGGGCCTGAATGACTGAATGTTCCCCGCCTGAGCTAACAGTCATGTG
 GGTGATTCACTCTGATGGATGTGTTCCAGAGCACAGAACAGAACAAATGTATATTCAAGAT
 AGACTGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
 ATCTCAGTGTGCCTATTGGCGCTTCCAGAACCGCGTACACTGATGGGGACATCTTATGC
 AATGATGGCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
 AATCCGCCTCAAAGGGAGAGCCAGGTGTTCAAGAACGGCGTGGTACTGCATGTGCTTCCAG
 AGGAGCCCAAAGAGCTCATGGCATGTGGTGGATTGATTGAGATGGATGTGTTTCCAG
 AGCACAGAAAGTAAACACGTGACCAAGGTAGAATGGATATTCAGGACGGCGCGCAAAGGA
 GGAGATTGTATTCGTTACTACCACAAACTCAGGATGTCTGGAGTACTCCCAGAGCTGGG
 GCCACTTCCAGAACCGTGTGAACCTGGTGGGGACATTTCCGCAATGACGGTCCATCATG
 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTACACCTGCAGTATCCACCTAGGGAACCT
 GGTGTTCAAGAAAACCATTGTGCTGCATGTCAGGCCGGAAGAGCCTCGAACACTGGTACCC
 CGGCAGCCCTGAGGCCTCTGGTCTGGTGGTAATCAGTTGGTATCATTGTGGAAATTGTC
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAACGACTGTGGAAATAA
 GAGTCAGTGAATTCTACAGTCTGGTGAAGAACACGAAGAACGACTAATCCAGAGATAAAAG
 AAAAACCTGCCATTGAAAGATGTGAAGGGAGAACACATTACTCCCCATAATTGTA
 CGGGAGGTGATCGAGGAAGAACCAAGTGAAGAACACATTACTGGGAAAGTCAGGTGGGG
 CCCAGTTGGCCTCTGAGGTCAAGTCAGATCGAACACTCACTGAAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTT**TGA**GAAGAACGAGACTCCCTCATCTCAGCAGCGG
 TGGAGACTCTCCTGTGTGTCTGGCCACTCTACAGTATTCAGACTCCGCTCTC
 CCAGCTGCTCCTGTCTATTGTTGGTCAATACACTGAAGATGGAGAACGGCTGG
 CAGAGAGACTGGACAGCTGGAGGAACAGGCCTGCTGAGGGAGGGAGCATGGACTTGGC
 CTCTGGAGTGGGACACTGCCCTGGAACCCAGGCTGAGCTGAGTGGCTCAAACCCCCGTT
 GGATCAGACCCCTCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAACAGAGATA
 AAAACCAACCCAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNSPPELTVHVGDSALMGCVFQSTEDKCI
FKIDWTLSPGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGT
YICEIRLKGESQVFKKAVVLHVLPEEPKELMVHGGLIQMGCVFQSTEVKHVTKVEWIFSGRR
AKEEIVFRYYHKL RMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRESDG
GNYTC SIHLGNLVFKKTIVLHVSPEEPRTLVT PAA LRPL VLGGNQLVII
VGIVCAT ILLPVL LILIVKKTCGNKSSVNSTV LVKNTKKT NPEI KEKPCH
FERCEGEKHI YSPII VREVIEEEPSEKSEATYMTMHPVWPSLR SDRNN
SLEKKSGGGMPKTQQAF

FIGURE 305

CTATGAAGAAGCTCCTGGAAAACAATAAGCAAAGGAAACAAATGTGTCCCATCTCACATG
GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTCGAAAGTCATTGAACCTCTGAGCTCAGTGCAGTACTCGGGAAGCCATGCA
GGATGAAGATGGATACATCACCTTAAATATTAAAACCGGAAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTGGTGGCGTGTGATGGCTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTCGGGCTGGTGGCTCTGGGATTGGTCTGTCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAATCGCACAGGAACCTTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAAACAATCAGAACTAAAGGGACTTCAAAGGTATAATGCAGCCCCGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTCAGGCACAACATTACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTAATTGTTGGCGATTATCTGCCAGAAGTCGAAT
GAGGTCTGGAAGTGGAGGATGGCTCGTTATCTCAGAAAATATGTTGAGTTTGGAAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTCATAATGGGAAATGCACCCCTACCTCTGTG
AGAACAAACATTATTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTATTGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAAA

FIGURE 306

MQDEDGYITLNKTRKPALSVGPASSSWRVMALILLILCVGMVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYGDSCYGFFRHNLNTWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLLIRWVGLSRQKSNEVWKWEDGSVISENMFEFL
EDGKGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

FIGURE 307

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCCTCCGCCTGCCAGTCTGCCCGCGATCCGG
 CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC
 CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTGCTGAAGCCCAGTGCAGGAGAA
 GCCCGGGCAAACGCAGGCTAAGGAGACCAAGCGCGAAGTCGCGAGACAGCGGACAAGCAG
 CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
 CGTCGTGGCC**ATG**GCAGCGGCTATGCCAGCTCGCTCATCCGTCAAGAAGAGGCAAGCCCGCG
 AGCGCGAGAAATCCAACGCCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
 GACAAAAACAAGTTAAATGTCTTCCCAGGCTAAACTCTCGGCTCCAAGAAGAGGCGCAG
 AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATAACAGCCGACAAGGCTACC
 ACTTGAGCTGCAGGCAGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACT
 CTGTTAACCTCATCCCTGTGGGTCTGCAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
 GTACTTGGCAATGAACAGTGAGGGATACTTGACACCTCGGAACCTTACACCTGAGTGCA
 AATTCAAAGAATCAGTGTGAAAATTATTATGTGACATATTCAATGATATACCGTCAG
 CAGCAGTCAGGCCAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
 CCATGTGAAGAAGAACAAAGCCTGCAGCTCATTTCTGCCTAAACCAACTGAAAGTGGCCATGT
 ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCGATCTGGAAAGCGGGACCCCAACC
 AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
G**TAG**CCAGTGAGGGCAAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
 TCTTCTAGCAGTCCTCACCCAAAAGTTCAAATTGTCAGTGACATTACCAAACAAACAGG
 CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASLIRQKRQAREREKSACKCVSSPSKGKTSCDKNKLNVFSRVKLFGSKKRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTKDEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGYLYTSELFTECCKFKEVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSQSGTPKSRSVSGVLNGGKSMHNEST
```

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGCCTGTATGCCATTATTGTTCTATGCTACTAGACATGGGGGG
 ACTTGGTAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTGGGGGGATTCAGTAAAAAGTGGGGATCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAACACCAAGGTTGGGTCCTCCTGACATTGGCAGTG
 CCCCAGTAGGGTGGGATGAGCGAATATTCCAAAGCTAAAGTCCCACACCCTGTAGATTAC
 AAGAGTGGATTGGCAGGAGTGTGCCAAAATACAGTGGAAAGGTGCCTGAAGATATTAA
 ACCACGTCTGGAAATTAGTGGTCTTGGCTTGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAAGGGACGTTTCAATAGGAGGCAAAACTCGAGGGTGGATCCACTGAGG
 AGTACATAGGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGTGGTACTGGCTGCT
 GTGGAGGGGGTACGTGAGGGGGGGTCTGGGCTTATCCTCAGGTCTGTGGTGGGCAG
 CGAGTCGGGCCTGAGCGTAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGAGCCCAG
 CGCGCTCGGGCGCCTGCCGGTTGGGGTGTCTCCTCCGGCGCT**ATG**GCGGCGCTGGC
 CAGTAGCCTGATCCGGCAGAACGGGAGGTCCCGAGGCCGGGGCAGCCGGCGTGT
 CGCAGCGCGCGTGTGTCCCCCGGCCACCAAGTCCCTTGCCAGAACGAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGCGGCCCGCGCGGCCGGACCGCGGCCGGAGCCTCA
 GCTCAAAGGCATCGCACCAAATGTTCTGCCGCCAGGGTTCTACCTCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCCAGAGGATAACCAGCTCCTCACCCACTCAACCTGATCCCT
 GTGGGCCTCCGTGGTCACCATCCAGAGCGCAAGCTGGTCACTACATGCCATGAATGC
 TGAGGGACTGCTACAGTCCGCATTACAGCTGAGTGTGCGTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCCTGCTCTACCGCCAGCGTCGTTCTGCCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCAGGTATGAAGGGAAACCGAGTTAAGAACCAA
 GGCAGCTGCCACTTCTGCCCAAGCTCCTGGAGGTGCCATGTACCAAGGAGCCTCTCC
 ACAGTGTCCCCGAGGCCTCCAGTCCCCCTGCC**TGA**AATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCCAGTGAGCCAGCCACCACAAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLQANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQAALKHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTAAAHLPLKLLEVAMYQEPLHSVPEASPSSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCCCATCGCTAGCGGTTGATCCGCCAGAACGGCAGGCAGGGAGCAGCACTGGACCGGGCTCTGCAACGGCAACCTGGTGGATATCTTCTCAAAGTGCGCATCTCGGCCTCAAGAAGCGCAGGTTGCCGCGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTTGCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACAATTCTACACTCTCAACCTCATACCAGTGGACTACGTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTATAAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTACCCCTGAATGCAAGTTTAAAGAATCTGTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAAACAGGAATCTGGTAGAGCCTGGTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGAGTAAAGAAAACCAAACCGCAGCTCATTCTACCCAAAGCCATTGGAAGTTGCCATGTACCGAGAACCATCTTGCATGATGTTGGGAAACGGTCCCGAAGCCTGGGTGACGCCAAGTAAAAGCACAAGTGCCTGCAATAATGAATGGAGGCAAACCAAGTCACAAAGAGTAAGACAACAT**TAG**

FIGURE 312

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503
><subunit 1 of 1, 247 aa, 1 stop
><MW: 27702, pI: 10.36, NX(S/T): 2
MAAAIASGLIRQKRQAREQHWRPSASRRSSPSKNRGLCNGNLVDIFSKVRI FGLKKRRLR
RQDPQLKGIVTRLYCRQGYYLQMHPDGALDGTKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
IAMNGEYLYPSELFPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASA IMNGGKPVNKS TT
```

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGTTGGGTGCCTGC
 AAAGGATGCAGGACGCAGCTTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTCTTGTGAGCCCTGGATCTAACACAAATGTATATGTGACACACAGGGAGCATTCAAGAATG
 AAATAAACCAGAGTTAGACCCGGGGGTGGTGTGTTCTGACATAAATAATCTAAAGCAGCTTCCC
 CTCCCCACCCCCAAAAAAAGGATGGAAATGAAGAACCGAGGATTCAAAGAAAAAGTATGTTCATTT
 TTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTGGAATGAAAAGTTGGGCTTTTAGTAAAGTAA
 AGAACTGGTGTGGTGGTGTTCCTTCTTTGAATTCCCACAAGAGGAGAGGAAATTAATAACATCTGC
 AAAGAAATTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAAACCAGCAGAGCA
 CAGTTGGATTGTCCTATGTTGACTAAAATTGACGGATAATTGCAAGTTGGATTTCATCACCTCCTT
 TTTTAAATTTTATCCTTTGGTATCAAGATCATGCGTTTCTCTGTTCTAACACACCTGGATTCCATCT
 GGATGTTGCTGTGATCAGTCTGAAATACAACACTGTTGAATTCCAGAACAGGACCAACACCAGATAAATTATGA**TG**
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTAACAGGCCCTATTGACCCCT
 GCTTGTGGTGTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTCTGTGT
 GCTCCTGCAGCAACCAGTCAGCAAGGTGATTGTGTTGGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCC
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTCAAGCACTTGAG
 GCACCTGGAAATCCTACAGTTGAGTAGGAACCATATCAGAACCATGAAATTGGGCTTCAATGGCTGGCGA
 ACCTCAACACTCTGAAACTCTTGACAATCGTCTTACCATCCCAGTGGAGCTTTGTATACTTGTCTAAA
 CTGAAGGAGCTGGTGCACACACCCATTGAAAGCATCCCTCTTACAGGTTAACAGAACCTCTT
 GCGCCGACTAGACTTAGGGAAATTGAAAAGACTTCATACATCTCAGAACGGTGCCTTGAAGGTCTGTCCA
 ACTTGAGGTATTGAAACCTTGCCATGTGCAACCTCGGGAAATCCCTAACCTCACACCAGCTCATAAA
 ACTGAGCTGGATCTGGGAAATCATTATCTGCCATCAGGCCCTGGCTCTTCCAGGGTTGATGCACCTCA
 GTGGGATGATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCCTGACAACCTCAGTCACTAGTGGAGATCA
 ACCTGGCACACAATACTAACATTACTGCCATGACCTCTCACTCCCTGCATCATAGAGCGGACAT
 TTACATCACACCCCTGAACTGTAACACTGTGACATACTGTGGCTCAGCTGGTGATAAAAGACATGGCCCC
 GAACACAGCTTGTGCCCCGGTAAACACTCCTCCAACTAAAGGGAGGTACATTGGAGAGCTGACCAGA
 ATTACTTACATGCTATGCTCCGGTATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCT
 GAGCTGAAATGTCGGCCTCCACATCCCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCATGACACA
 TGGGGCGTACAAAGTGGGAGACTGTGCTCAGTGATGGTACGTTAACATTGACAAATGTA
 ACTGTGCAAGATA
 CAGGCATGTACACATGTATGGTGGTAATTCCGTTGGAAACTACTGCTTCAGCCACCTGAATGTTACTGCA
 GCAACCAACTCCTTCTTACTTTCAACCGTCACAGTAGAGACTATGAAACCGTCTCAGGATGAGGCACG
 GACCACAGATAACAATGTGGGCCCCACTCCAGTGGTCAGTGGAGACCACCAATGTGACCACCTCTCACAC
 CACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGA
 CTGACTGATATAAACAGTGGGATCCCAGGAATT
 GATGAGGT
 CATGAAGACTACCAAAATCATCATTGGGTGTTGTGGCCATCACACTCATGGCTGCAGTGATGCT
 GGTCA
 TTTCTACAAGATGAGGAAGCAGCACCACGGCAAACCATCACGCCCAACAAGGACTGTTGAAATT
 TTAATGTGGATGAGATTACGGGAGACACACCCATGAAAGCCACCTGCCATGCC
 GCTATCGAGCATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCCTCAACCACACAACAGTAA
 CACACAATGAC
 CAGTTCA
 GTCAGTGCATGAACCGTTATTGATCCGAATGAACTCTAAAGACA
 ATGTA
 CAGAGACTCAAATCTAAACAA
 TTTACAGAGTTACAAAAACAA
 ATCAAAAAAGACAGTTATT
 TAAAAATGACACAAATGACTGGGCTAA
 ATCTACTGTTCA
 AAAAGTGTCTTAC
 AAAAGAAAAAGAAA
 AGAAATT
 TATT
 TATT
 AAAATTCTATTG
 TGATCTAAAGCAGACAAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNRALFDPLLVVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
 VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
 YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLPHDLFTPPLHHLERIHLHHNPWCNCIDIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
 LKCRASTSLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVSNSVGN
 TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
 STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
 HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHNSYKSPFNHTTVNTINSIHSS
 VHEPLLIRMMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
434-438, 442-446, 488-492, 606-610**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCCCATCTGCCCGAGGGCACGGGGCGCGGGGCGGGCTCCGCCGGCACAT
GGCTGCAGCCACCTCGCGCGACCCCAGGGCAGCGCCAGCTGCCAGGTCGTGGAG
GGCGCCCGGCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCTCCGGGATC
GGG**TG**TCCTCCTCTCTTGCTAGTTCTACTATGTTGAAACCTGGGACTCA
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTGCCCTGCCACCATAACTGGGC
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGTCACCGATAATGAAGGAAACAAAAA
GTGGTGTACACTTACTCCAGTCGTATGTCATAACTGACTGAGGAACAGAACGGCCG
AGTGGCCTTGCTTCCAATTTCCTGGCAGGAGATGCCCTTGCAAGATTGAAACCTGTGAAGC
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAAGGGCCTACGTGTGGAGGCCAT
GTCATCTAAAAGTCTTAGTGAGACCATCCAAGCCAACTGAGTTGAAAGGAGAGCTGAC
AGAAGGAAGTGACCTGACTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCATTGTGATT
ACTGGCAGCGAATCCGAGAGAAAAGAGGGAGAGGATGAACGTCGCCCTCCAAATCTAGGATT
GACTACAACCACCCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA
CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCAGTAAGTACAGT
ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
ATTTTCTCTGGGTGTGGCTGCTAATCCGAAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
GAGACCTAATGAAATTGAGAAGATGCTGAAGCTCCAAAAGCCGTCTGTGAAACCCAGCT
CCTCTCCTCAGGCTCTGGAGCTCACGCTCTGGTTCTTCCACTCGCTCCACAGCAAAT
AGTCCTCACGCCAGCAGGGACACTGTCAGTGACGCAGCACCCAGCCAGGGCTGGCCAC
CCAGGCATACAGCCTAGTGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG
CTAATCTGACCAAAGCAGAAACACACCCAGCATGATCCCCAGCCAGAGCAGACCTTCAA
ACGGCT**TGA**ATTACAATGGACTTGACTCCCAGCTTCTAGGAGTCAGGGCTTGGACTC
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA
GTGAGCATTGCACGGAACAGATTCAAGATGAGCATTTCCTTACAATACCAAACAAGCAA
AGGATGTAAGCTGATTCATCTGAAAAAGGCATCTATTGTGCTTAGACCAGAGTAAGGG
AAAGCAGGAGTCCAAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGAAAGGTG
AGGTGAATATACTAAACTTTAATGTGGATATTGTATCAGTGCTTGATTCAAATT
TTCAAGAGGAAATGGATGCTGTTGTAATTTCATGCAATTCTGCAAACATTATTGGATT
ATTAGTTATTCAAGACAGTCAGCAGAACCCACAGCCTTATTACACCTGTACACCATGTAC
TGAGCTAACCACTCTAAGAAACTCCAAAAAGGAAACATGTCCTCTATTCTGACTAAC
TTCATTGTCATAAGGTTGGATATTAAATTCAAGGGAGTTGAAATAGTGGAGATGGAGA
AGAGTGAATGAGTTCTCCACTCTATAACTATCTCACTATTGTATTGAGCCAAAATAAC
TATGAAAGGAGACAAAATTGTGACAAAGGATTGTGAAGAGCTTCCATCTCATGATGTT
ATGAGGATTGTTGACAAACATTAGAAATATAATGGAGCAATTGTGGATTCCCTCAAAT
CAGATGCCTCTAAGGACTTCTGCTAGATAATTCTGGAAAGGAGAAAATACAACATGTCAATT
TATCAACGTCTTAGAAAGAATTCTCTAGAGAAAAGGGATCTAGGAATGCTGAAAGGATTA
CCCAACATACCATTATAGTCTCTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTCTCTTAATATGTCAAGGAAGGTAGCCGGCA
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

FIGURE 316

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41281, pI: 8.33, NX(S/T): 3
MSLLLLLLVSYYVGTGHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPCKELEGELTEGSDLTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMYSGLYQCTAGNEAGKESCVVRTVQYVQSIGMAGAVTGIVAGALLI
FLLVWLLIRRKDERYEEEERPNEIREDAEAPKARLVKPSSSSGSRSSRGSSSTRSTANS
ASRSQRTLSTDAAQPGLATQAYSLVGPEVRGSEPKVHHANLTKAETTPSMIPSQSRAFQTV
```

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

CGCGAGGCCGGGAGCCTGGACCAGGAGCGAGAGCCGCACCTGCAGCCGCCAACGGCACGGCAGCCA
 CC**ATG**GCGCTCTGCTGTGCTTCGTGCTCTGTGCGGAGTAGTGGATTGCCAGAAGTTGATATCACTACT
 CCTGAAGAGATGATTGAAAAAGCAAAGGGAAACTGCCTATCTGCCATGCAAATTACGCTTAGTCCCAGAAGA
 CCAGGGACCGCTGGACATCGAGTGGCTGATATCACCAAGCTGATAATCAGAAGGTGGATCAAGTGATTATTTAT
 ATTCTGGAGACAAAATTATGATGACTACTATCCAGATCTGAAAGGCCAGTACATTACAGTAATGATGATCTC
 AAATCTGGTGTGATGCATCAATAATGTAACGAATTACAACACTGTCAAGATATTGGCACATATCAGTGAAAGTGA
 AAAAGCTCTGGTGTGCAAATAAGAAGATTCATCTGGTAGTTCTGTTAACGCTCAGGTGCGAGATGTTACG
 TTGATGGATCTGAAGAAATTGGAAGTGACTTTAAGATAAAATGTGAACCAAAAGAAGGTTCACTTCCATTACAG
 TATGAGTGCAAAATTGCTGACTCACAGAAAATGCCACTCATGGTTAGCAGAAATGACTTCATCTGTTAT
 ATCTGTAAGGAAATGCCCTTCTGAGTAECTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGCTCTGATC
 AGTGCCTGTTGCGTCTAAACGTTGTCCTCCTCAAATAAGCTGGACTAATTGCAAGGAGCCATTATAGGAAC
 TTGCTGCTCTAGCGCTATTGGCTTATCATCTTGTGCTGTAAGGAGCCAGAGAAAATATGAAA
 GGAAGTTCATCAGATCAGGAAAGATGCGCACCTCCAAAGAGCGTACGTCCACTGCCAGAAGCTACATCG
 GCAGTAATCATTCCCTGGGTCATGTCCTCCAAACATGGAAGGATATTCAAGACTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAACGCCTCTCAGACTCGACTCTCCACCTGCTAAGTCAAGTACCCATTACAA
 GACTGATGAAATTACAGTTGTA**TAA**ATATGGACTACTGAAGAATCTGAAGTATTGATATTGACTTTATT
 AGGCCTCTAGTAAAGACTTAAATGTTTAAAAAGCACAAGGCACAGAGATTAGAGCAGCTGAAAGAACAC
 ATCTACTTTATGCAATGGCATTAGACATGTAAGTCAGATGTCATGTCAAAATTAGTACGAGCAAATTCTTGT
 TAAAAACCCATATGATAGTGCACACTGATAGTTAAAGATGTTTATTATATTTCATAACTACCAACTAACAA
 ATTGTTAACCTTATGCAATTCTGATATGTTAGGAAAGTATGGTTAATAGTTGATTTCAA
 AGGAAATTAAAATTCTACGTTCTGTTAATGTTTGCTATTAGTTAATACATTGAAGGAAATACCG
 TTCTTCCCTTATGCACACAACAGAAACACGCGTTGTCATGCCAAACTATTGCAACTACA
 TGATTTCACACAATTCTCTAAACAACGACATAAAAGATTCTCTGTATATAAAACTACATACGCTCA
 TAAAGTAATTCTCAAAGGTGCTAGAACAAATCGCCACTCTACAGTGTCTCGTATCCAACAGAGTTGATGC
 ACAATATATAAACTCAAGTCCAATTAAAATTAGGCACTGACTAACCTTAATAAAATTCTCAAAC
 TATCAATATCTAAAGTCATATTTTAAGAAAGATTATTCTCAATAACTTCTATAAAATAAGTTGATGG
 TTTGGCCCATCTAACCTCACTACTATTAGTAAGAACCTTTAACCTTTAATGTTAGTAAGGTTATTCTACCTT
 TTTCTCAACATGACACCAACACAATCAAAACGAAGTTAGTGAGGTGCTAACATGTCAGGATTAACTCCAGTGAT
 TCCGGTCACAATGCATTCCAGGAGGAGTACCCATGTCAGTGGAAATTGGCGATATGGTTATTCTTCTCCC
 TGATTTGGATAACCAAATGGAACAGGAGGAGTAGTGATTCTGATGCCATTCCCTGATACATTCCCTGGCTT
 TTTCTGGCAAAGGGTGCACATTGGAAGGAGGTGAAATATAAGTTCTGAAATCTGTAGGGAAGGAGAACACAT
 TAAGTTAATTCAAAGGAAACATCATCATCTATGTTCCAGATTCTCATTAAAGACAAAGTTACCCACAACACT
 GAGATCACATCTAAAGTCACCTCTATTGTCAGGTCTAAATACATTAAAACCTCATGTCATAGGCGTATAA
 TGTATAACAGGTGACCAATTGTTCTGAATGCATAAGAAAGATTGAAATAACTCAAACACAGTACTTCTAAACAA
 CTTCAACCAAAAAAGACCAAAACATGGAACGAATGGAAGCCTTGTAAAGGACATGCTTGTGTTAGTCCAGTGGTT
 CCACAGCTGGCTAACGCCAGGAGTCACCTGGAGGCTTTAAATACAAACATGGAGCTGGAGGCCATTATCCTT
 AGCAAACACTAATGCAGAAACAGAAAATCAACTACCGCATGTTCTACTTATAAGGGAGGTAATGATAAGAACT
 TATGAACACAAAGAAGGAAACAATAGACATTGGAGTCTATTGAGAGGGAGGGTGGGAGAAGGAAAGGAGCA
 GAAAAGATAACTATTGAGTACTGCCTTCACACCTGGGTGATGAAATAATATGTCACACAAATCCCTGTGACACA
 TGTTTACCTATGGAACAAACCTTCATGTCATGTCATCCCTAAACCTAAAATAAAAGTTAAAAAAAAAAAAA
 AA
 AAAAAAAAAAAAAAAAAA

FIGURE 318

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361
><subunit 1 of 1, 352 aa, 1 stop
><MW: 38938, pI: 7.86, NX(S/T): 3
MALLLCFVLLCGVVDFARSLISITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCYVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSDQCLRLNVVPPSNKAGLIAGAIIGTILL
ALALIGLIIIFCCRKKRREEKYEKEVHHDIREDVPPPRTSTARSYIGSNHSSLGMSMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV
```

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA
 ATGGTGAAGGTGCCTGTCTAACCTTTCTGTAAAAAGAACCGAGCTGCCTCAGGCAGCCAGCC
 CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTCGC
 CAATTAAACACCAAGAAGAATTGAGGCTGCTGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTGCCCTC
 CTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTGCCTGGGTTTACCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTGGGCCCTGCCAAGT
 GAAGGGGTTGTTCCCCAGAAACTGTGGGAAGCCTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACGAGTGCCCGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCCCTGCTGGAGTTCTACTGAAAAGTGTGTTCAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTACTCTGCCAACAACT
 TTGTTCTCATCGTGTACAACAGTCAAGAAAATGAGATGTTCCATCAGAGAC
 AGTGCACACAGGCGGTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAACGAGC
 TCTGACCAAAGCCCTGGGAAGTGGACATTCTCTGACCTGGATGCAGAAATTCTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTGTTCCCTGTGTCATTCA
 AACAGTCTCCCTTCTATGCTGTTCACTGGACACTTCACGCCCTGGCCATGGTCCCATT
 TTGGCCCAAGGATTATTGTCAAAGAACAGTCATTCTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTGTATTATTACAACCTATT
 AATTAATGTCAGTATTCAACTGAAGTTCTATTATTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCATGCTTCTTACCCCTACAATCCTGCCACAGTGTGGGCAG
 TGGATGGGTGCTTAGTAAGTACTTAATAACTGTGGTGCTTTGGCCTGTCTTGGATT
 GTTAAAAAACAGAGAGGGATGCTGGATGTAAAAGTCAACTGAGCATGAAACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGTGGGGTAAGGTGCATCTGTTGAAAAG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTCA
 TCCCACCCACACTGCCAGCTCACCCATCATCCCTTCCCTGGTGCCCTCCTTTTT
 TATCCTAGTCATTCTCCCTAATCTCCACTGAGTGCAAGCTGACCTGCTGATGGTGAC
 ATTGCACCTGGATGTTACTATCCAATCTGTGATGACATTCCCTGCTAATAAGACAAACATAA
 CTCCAAAAAAAAAAAAAAAAAAAAAA

320/330

FIGURE 320

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002
><subunit 1 of 1, 206 aa, 1 stop
><MW: 23799, pI: 9.12, NX(S/T): 3
MNFQQRLQSLWTLARPFCPPLLATASQMQMVVLPCLGFTLLLWSQVSGAQGQEFGFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL
```

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTCCCTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTC
CACAGACATGCACCATATAGAAGAGAGTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGAACAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTCAAGGATCA
TCAGGAGCCAACCCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTCCTCTACA
TGCAGAAAATCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAAGAGTCATCCATGACAACATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAAGTGTGATCCAGGGATGAACACCCCCCTGTGCGGTTACT
GTGGGAGACAGCCCACCTTGAAGGGGAAGGAGATGGGGAAAGGCCCTTGAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAGTCTACTGTGGTAT
TTGTAATAAAACTCTATCTGCTGAAAGGCCTGCAGGCCATCCTGGAGTAAAGGCTGCCTT
CCCATCTAATTATTGTAAAGTCATATAGCCATGTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTCTGAATAAATTCCATATTTACCTATGA

FIGURE 322

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVNDHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQRQCHCRQEATNATRVIHDNYDQLEVHAAAIKSLGELDVFLAWINKHEVMFSA
```

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCACTGGCTTCGTTAG
AACGCGGCTACAATTAATAACATAACCTTATGTATCATACACATACGATTAGGTGACACTAT
AGAATAACATCCACTTGCCTTCTCTCCACAGGTGTCCACTCCCAGGTCCAAC TGCACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCGCCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCA
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCA CCTGCAGATCCACAAGAATGGCATGTGGATGGC CACCCCATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTGTGGTATTACAGGTGTGA
TGAGCAGAAGATA CCTCTGCATGGATTCAGAGCAACATTGGATCACACTATTCGAC
CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC
TCAGTATCACTCCTGGTCAGTCTGGCCGGCGAAGAGAGGCCTCCTGCCAGGCATGAACC
CACCCCCGTACTCCCAGTTCCGTCCCAGGAAACGAGATCCCCCTAATTCACTTCAACACC
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCAGGGACCCCTGAACGT
GCTGAAGCCCCGGGCCGGATGACCCGGCCCGGCTCCTGTTCACAGGAGCTCCGAGCG
CCGAGGACAACAGCCCAGGCCAGTGCACCTAGGGGTGGTCAGGGCGGTGAGTGAAC
ACGCACGCTGGGGAACGGCCCGGAAGGCTGCCGCCCTCGCCAAGTTCATCTAGGGTCG
CTGG

FIGURE 324

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238
><subunit 1 of 1, 251 aa, 1 stop
><MW: 27954, pI: 9.22, NX(S/T): 1
MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPSQFLSRRNEIPLIHFNTPIP RRHTRSAEDDSE
RDPLNVLKPRARMTPAPASC SQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA
KFI
```

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGTCTGGCTCTGCCCTTCTTCTGCTGGAGGTTGGGTCTCTGG
 GAGCTCTGCAGGCCAGCACCGCAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCTCTTAGGGCCTAACCCCCAGCCGCCATTCCAGAACGAGAGACCAGGGAGCCA
 GAGAATTCCCCTGCAAGAGAGACCAGGAGTTCACAAAAACATCTCCAACTTCATGGTGC
 TGATGCCACCTCCGTGGAGACATCAGCCGCAGTGGCAGGCCAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCAGGAAGCCATTTGACACCCCTTGACCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCTGTCTCAGAGAGCAGTCGCTCTCCGACGCCCATCCAGTCATC
 ACCCGTCACGGCCTCAGAGAGCAGCGCTCTCCGACGCCCATCCAGTCATCACCC
 GTCACGGCCTCAGAGAGCAGCGCTCTCCGACGCCCATCCAGTCATCACCC
 GGTCCCCGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTACTGTCACAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTCCAGCATCCCTGGGCCTCAGA
 CATAGATCTCATCCCCACGGAAGGGTGAAGGCCTCGCACCTCGATCCACAGCTCTGC
 CTGACTCCACTGAAGCAAACACACATCACTGAGGTACAGCCTCTGCCGAGACCCGTCC
 ACAGCCGGCACCAAGAGTCAGCTGCACCTCATGCCACGGTGGGACCCACTCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGAAGCAGCAGCACCCGGGCCACGACCCCTCAGTGGAGCTGGTCA
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTGTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCGGTCTCCATAGAGGCTGGTCAGCAGTGGCAAAACAACCTC
 CTTGCTGGAGCTCTGCTCCTCCTACAGCCCTCGGAAGCCCTCAAGAACCTCACCC
 CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGCCTTCCCCACCAGCAGGGACCC
 CTTCTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTAGCCAA
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCGGAC
 GAGGCCGACCACAGACG**TGA**GTGCAGGTGAAATGGAGGTTCCCTCCTGCGGCTGAGTG
 TGGCTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACTCCACGCCACGCGCTCACTCCAGGTCTCCTACTGCGTGTAGGAGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCGTATGCCAAAAGAGGGTGTGCCCCTAGCCTG
 GGCCCCCACCAGACAGACTGCAGCTCGTTACTGTGCTGAGAGGTACCCAGAAGGTCCCAG
 AAGGGCAGCATGTCCAAGCCCTAACCCAGATGTGGAACAGGGACCCCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGGAGGGGCTCACCTGTTCCAGAGGTGTGACTCACCTTGG
 CACATGTTCTGTGTTCAAGAAAGAGAGACCTGATCACCCATCTGTGCTTCCATCTGCA
 TTAAAATTCACTCAGTGTGCCCAAAAAAAA

FIGURE 326

MGCLWGLALPLFFFCEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTLSA
ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSPNFMVLIAVTSAASGSPEGAGM
TTVQTITGSDPEEAIFDTLCTDDSSEEAKTLTMDILTLAHTSTEAKGLSSESSASSDGPHPV
ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEALVTVTNI
EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTS DPPALPDSTEAKPHITEVTASAETL
STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLS GALVTVRNPLEETSALS VETPSY
VKVSGAAPVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGPFPTS RD
PLPSVPPTTNSSRGTNSTLAKITTSAKTTMKPQQPRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP-and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTCGGGCTCGCCGAGACCCCCGCGCGGATTCGCCGGCCTTCCCGCGG
 GCGCAGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGCGCCGGGTCCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCAGCCTCTAAAGCAAATAAGACCAGAGGGAGGATTAT
 CCTTGACCTTGAGAACCAAAACTAAACTGAAATTAAA**ATG**TCTCGGGGGAGAAGGGAG
 CTTGACTTACACTTGGTAATAATTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTGTGATGACATCCAGTCATCTCTTCTAAGGAATC
 AGAGGCAATGAGCCCCTATATACTTCAACTCAAGAAGACTGCATTAATTCTGCTGTTAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACGTACCTATTTCATGGCCAATTTCACAAGCAGTCACACTCCCC
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTCATCTTGCACAGAAATTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTTACATGGCCAATTTCACAAGCAGTCACACTCCCC
 TAGCCCACATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTGGATCCTCAGATCACCTGGAGAAACTATTAAAGATGGATGAAGCAAGTGCCA
 GCTCCTGCTTATAAGGAAAAGGCCATTCTCAGAGTCACAATTTCCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTCTCCA
 CATACCACCTCGGCTACTCCAAAGCCCACCCCTCTACCCACCAATGCTCAGTGACACC
 TTCTGGGACTTCCAGCCACAGCTGCCACACAGCTCCACCTGTAACCACACTGTCACCTCTC
 AGCCTCCCACGACCCCTCATTCACAGTTTACACGGGCTCGGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCAGTTACAGAAATCTCAAACCTTAACCTTGAAACACAGGGAATGTGTATAACCTA
 CTGCACTTCTATGTCAAATGTGGAGTCTTCACTATGAATAAAACTGCTCCTGGAGGTT
 AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTCCAGAAAATCAGTACGGCCTTCC
 ATTTGAAAATGGCTTCTTATCGGGCCCTGCTTTGGTGTCTGTTGGTGTAGGGCCTTCC
 TCGTCCTCCTGGTAGAACCTTCCGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT
 TATTGATCAATGGATCTATGTGGACAT**TAA**AGGATGGAACTCGGTGTCTTAATTCTT
 TAGTAACCAGAACGCCAAATGCAATGAGTTCTGCTGACTGCTAGTCTTAGCAGGAGGTTG
 TATTGAAAGACAGGAAATGCCCTCTGCTTCCCTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCAGTCGGCTCTCACCGCAACCTCCGTCTC
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTATTGGTATTCTGCTTGTAGAGAGACGGGTTTACCATGTTGGTCAGGCTG
 GTCTCAAACCTGACCTAGTGATCCACCCCTCTGGGCTCCAAAGTGCCTGGGATTACAGG
 CATGAGCCACACAGCTGGCCCCCTCTGTTTATGTTGGTTTGAGAAGGAATGAAGTG
 GGAACCAAATTAGGTAATTGGTAATCTGCTCTAAATATTCAAACACTGGCTTTATGCAA
 ATGTAAGTAATAAGTATAATTGCCATATAAATTCAAACACTGGCTTTATGCAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCACTCACATTCTGGTCCAGATAAAACTTATT
 TGTTTATGCAAATTCTAATGGATTGCTTTCTTTATATGGATTCCCTTAAACTTATT
 CCAGATGTAGTCCTCCAATTAAATATTGAATAATCTTTGTTACTCAA

FIGURE 328

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVIICFLRLSASQNCLKKSLEDVVIDIQSSLKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATILL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMNSNVESSTMNKTAWEGRASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSES LRRKRYSRLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCCACGGTGTCCAGGCCAGA**ATGCGGCTCTGGCTCTGCTATGGGTTGCCTGCTGCT**
 CCCAGGTATGAAGCCCTGGAGGGCCCAGAGGAATCAGCGGTTGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAAGAGCTGAGGGACCACCGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTCTCGCTGCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCAGGAGCTCTCGCTATTGTGACCCCTGTGGA
 ACCTCACCTGCAAGACGCTGGGAGTACTGGTGTGGGTCGAAAAACGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTCGTCTTCCAGGACCTGCTGTCCCTCCCTCTCCCAC
 CTTCCAGCCTCTGGCTACAACACGCCAGCAGCCAAAAGCTCAGCAAACCCAGCCCC
 CAGGATTGACTCTCCTGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGAAAGACAGGG
 GCTGAGGCCCTCCATTGCCAGGGACTTCCAGTACGGCAGCAGAAAGGACTCTCAGTACAC
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCGCCCCCCCATGCAGC
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCAGCAGTGGCAGCTCTAAGCCCAGG
 GTGTCCATCCGATGGTCCGCATACTGGCCCCAGTCTGGTGTGCTGAGCCTTGTGTCAGC
 CGCAGGCCTGATCGCCTCTGCAGCCACCTGCTCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGAACGAGAACAGTTCTGGCTCTACGCTTGACTGCGGAGGAAAGGAAGCC
 CCTTCCCAGGCCCTGAGGGGAGCTGATCTCGATGCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTGTCTCAGCG**TAG**GGCAGGAGGCCCTCTGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTCCACCTCAGCCTCAGAG
 TCCAGCTGCCGGACTCCAGGGCTCTCCCCACCCCTCCCCAGGCCTCTCCTTGCATGTTCCA
 GCCTGACCTAGAACGTTGTCAAGCCCTGGAGGCCAGAGCGGTGGCCTGCTCTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTCACATCCCTGGCAGAGTACCAAGGCTGCTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTCAATCTGCCAGGAACCTGGC
 CTCATGCCAGTGTGGACCTGCCCTGCCTCTCCACTCCAGACCCCACCTGTCTCCCTCCC
 TGGCGTCCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGTGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTCTTTGAACCACCTGCATCCAGCCCTCAGGAAGCCT
 GTGAAAAACGTGATTCTGGCCCAACCAAGACCCACAAAACCATCTCTGGCTGGTGCAG
 GACTCTGAATTCTAACAAATGCCAGTGAATGTCGCACTTGAGTTGAGGGCCAGTGGGCTG
 ATGAACGCTCACACCCCTCAGCTTAGAGTCTGCATTGGCTGTGACGTCTCCACCTGCC
 CAATAGATCTGCTCTGCGACACCAGATCCACGTGGGACTCCCTGAGGCCCTGCTAAG
 TCCAGGCCTTGGTCAGGTCAAGTGCACATTGCAAGGATAAGCCCAGGACGGCACAGAAGTGG
 TTGCTTNCATTGCCCTCCCTGGNCCATGCCTTGTGCTGGAAAAAATGATGAAGA
 AACCTGGCTCTTGTCTGGAAAGGTTACTTGCTATGGGTTCTGGTGGCTAGAGA
 GAAAAGTAGAAAACCAGAGTGCACGTAGGTGTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAAGGGTCGGGGTGGTAAAGTA
 GCACAACACTATTCCCCCTTCCATTATTATTGTTTTAAGACAGAAATCTCGTGT
 GCTGCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACCTCCGCCCTGGTTCAAGTGATT
 CTTCTGCCCTCAGCCTCCGAGTAGCTGGATTACAGGCACGCACCACACCTGGCTAATT
 TTTGTACTTTAGAGATGGGTTTACCATGTTGCCAGGCTGGTCTTGAACCTGAC
 CTCAAATGAGCCTCCTGCTCAGTCTCCAAATTGCCGGATTACAGGCATGAGCCACTGTG
 TCTGCCCTATTCTTTAAAAAGTGAATTAAGAGTTGTTCAAGTATGCAAACCTGGAAAG
 ATGGAGGAGAAAAGAAAAGGAAGAAAAAAATGTCAACCATAGTCTCACCAGAGACTATCAT
 TATTCGTTTGTGTACTTCCACTCTTCTTCACTATGACATGAGGAAATTTGCGGTGTTCTT
 TTTACAGAGCAATTATCTGTATATACAACCTTGATTCCTGCCCTTCCACCTTATCGTTCC
 ATCACTTATTCCAGCACTCTGTGTTACAGACCTTTATAAAATGGTCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196
<subunit 1 of 1, 332 aa, 1 stop
<MW: 36143, pI: 5.89, NX(S/T): 1
MRLLVLLWGCLLPGYEALEGPEEISGFEGDTVSLQCTYREELDHRKYWCRKGGLFSRCS
GTIYAAEEGQETMKGRVSIRDSRQELSLIVTLWNLTIQDAGEYWCGVEKRGPDESLLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTAEDTSPALSSGSSKPRVSIPMVR
LAPVLVLLSLLSAAGLIAFCSHLLWRKEAQQTETQRNEKFWSRLTAEEKEAPSQAPEGD
VISMPPLHTSEELGFSKFVSA
```

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128